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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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GTGGCGCTGAGCACTGCGCTATTTAACAATGGATTAAGTTGTGGTGCTTGCT		GGAGCT		recre	<u> </u>	CLASSIFICATION: 530 CHASATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 681 TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE TOPOLOGY: UNKNOWN )8-440-517A-1	PERFECT ON DATA	PORM:	STATE	SEE: PENNSYLVANIA: 113 TECHNOLOGY COUNIVERSITY PARK PENNSYLVANIA	SS: 6 DRESS: LLECTU	JUN V: PURIF	OVE, DA INAN, N RBAN, 1	ion US/			152331	1762 72604	1762 1762 1762	246240 246240 5852	580073 1305 246240	277 277 99500	248
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TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1994-05-12
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APPLICANT: COSGYOVE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
                                Query Match
Best Local Similarity 100:0%;
Matches 681; Conservative
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RESULT 3
US-08-845-539-5
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APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific
TITLE OF INVENTION: Expansin Genes
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHETIN Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
                                                                                                                                               ADDRESSEE:
STREET: Tw
CITY: San
                                                                                                               STATE: California COUNTRY: USA
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US-09-362-642-5

; Sequence 5, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
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TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 537 base pairs
TYPE: nucleic acid
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Best L
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                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
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OTHER INFORMATION:
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es 380; Conserv
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CANT: Bennett, Alan B.
CANT: Rose, Jocelyn K.C.
CANT: The Regents of the University of California
CANT INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
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                                                                                                                                                                                                                                                                                                                              CTCTTCCTAATGACAATGGCGGTTGGTGAACCTTCCTCGCACTCATTTCGACCTCGCTA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTCCCTAACAACAATGGTGGATGGTGCAACCCTTCTCCAACACTTCGACATGGCTG 541
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Pred. No. 2.4e-74;
D; Mismatches 146;
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US-07-885-970A-6

Sequence 6, Application US/07885970A
Patent No. 5495070
GENERAL INFORMATION:

APPLICANT: John, Maliyakal TITLE OF INVENTION: GENETIC NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS:

GENETICALLY

ENGINEERING COTTON

M

STREET: F.C CITY: Madison CTATE: Wisconsin

ADDRESSEE:

E: Nicholas J. P.O. Box 2113,

Seay, First

Quarles & Wisconsin

Brady Plaza

COMPUTER READABLE FORM:

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I LENGTH: 537

I TYPE: DNA

ORGANISM: Cucumis melo
EBATURE:
NAME/KEY: CDS
I LOCATION: (1)..(537)
OTHER INFORMATION: melon expansin (C)
US-09-362-642-5
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: to Control Fruit Texture FILE REFERENCE: 023070-078210US CURRENT APPLICATION NUMBER: US/09/362,642 CURRENT FILLING DATE: 1999-07-27 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                          485 GATCAAACACCGGTTGGATGAGCATGAGTCGTAATTGGGGGCCAAAACTGGCA
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                                                                                                                                                                                                                                                                                             CTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCCTCTCCAACACTTCGACATGGCTG
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                                                                                                  ATTTGGTGTTAATCACCAACGTCGCGGGTGCAGGGGATATCGTGAGGGTCAGCGTAAAAG
                                                                                                                                                                                       TGCCTATGTTCCTCAAGATCGCTGAGTACCGCGCTGGGAATCGGACCTGTCTTTACCGCC
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71.4%;
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Pred. No. 2.4e-74;
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J.RAIN: Gossypium hirsutum
J.RAIN: Coker 312
DEVELOPMENTAL STAGE: 10 day old f
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKFB10
CLONE: B12
US-07-885-970A-6
Querv M
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INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0'
FILING DATE: 04-OCT-1988
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APPLICATION NUMBER: US 07/617,239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27,386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Word
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  862 TCCAATTGGCAATTTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCA 910
                                                                                                                                                                       742 TCCATGTCTAGAAATTGGGGCCAAAACTGGCAAAGCAACAACTATCTCAATGGCCAAGGC
                                                                                                                                                                                                                                                                                                                                       622 GGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                         562 GCTCAATACCGAGCTGGTATCGTCCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 ATTAGGGTCACTGCCAACTTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAACGATGGT
                                                                                                                                                                                                                                                                    682 GTCGGTGGCGCAGGCGACGTCCACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGGTGGTGCAATCCCCCACGAGAACACTTTGATTTTGGCCGAACCGGCATTCTTGCGGATA 120
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                                                                                                      CTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCACTGCCTATAATCTCGTTCCT
                                                                                                                                                CCTATGTCCAGAAATTGGGGCCAAAACTGGCCAGAGCAATGCTTAACCTTAACGGACAAAGC
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Pred. No. 4.5e-70;
0; Mismatches 129
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US-08-298-687A-6
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Best Local Similarity
                                                                                                                                                                                                                              Matches 340;
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: 10 or TISSUE TYPE: fiber cells IMMEDIATE SOURCE: LIBRARY: CKFB10 CLONE: B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPULOUS TYPE: CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 04-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 GCTGGTTGGCAATTCGGACAAACTTTTGAAGGAGGCCAGTTTTAAGACA 469
562 GCTCAATACCGAGCTGGTATCGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAA
                                                                                                                                                                                        442 ATTAGGGTCACTGCCACCAACTTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAACAATGGT
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                                                                                                      ATAACCGTGACAGCCAACTTTTGTCCACCTAACTATGCTTATCTAGTGACAATGGC 60
                                                                 GGGTGGTGCAATCCCCCACGAGAACACTTTGATTTGGCCGAAACCGGCATTCTTGCGGATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wisconsin
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                                                                                                                                                                                                                                Conservative
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72.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                              10 day old fiber cells
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Pred. No. 4.5e-70;
0; Mismatches 129;
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Patent No. 5597718
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
APPLICANT: Umbeck, Paul F.
                                                                                                                               REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: E
SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/617,239
FILING DATE: 21-NOV-90
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-88
ATTORNEY/AGENT INFORMATION:
                                          ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
ORGANISM: Gossypium
STRAIN: Coker 312
DEVELOPMENTAL STAGE:
                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/530,797 FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette - 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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P.O BOX 2113
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Umbeck, Paul F.
Brill, Winston J.
BYILL GENETICALY ENGINEERED COTTON PLANTS
VENTION: FOR ALTERED FIBER
BQUENCES: 18
                             Gossypium hirsutum
                                                                                                         linear
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                                                                                           cDNA to mRNA
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   10 day old fiber cells
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; TISSUE TYPE: fi
; IMMEDIATE SOURCE:
;; LIBRARY: CKFB10
; CLONE: B12
US-08-530-797-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08298829
Patent No. 5620882
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/885,970
                 FILING DATE: 18-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                           SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J.
STREET: P.O. Box 2113,
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                          STATE: W
                                                                                                        APPLICATION NUMBER: US/08/298,829 FILING DATE: 19-OCT-1994
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 CITY:
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                                                                                                                                                                                                                                                                                             Wisconsin
                                                                                                                                                                                                                                                                            USA
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72.5%;
US 07/617,239
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Pred. No. 4.5e-70;
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RESULT 9
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TISSUE TYPE: fiber cells

IMMEDIATE SOURCE:

LIBRARY: CKFB10

CLONE: B12

US-08-298-829-6
                                                                                          US-08-787-335-5
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Sequence 5, Application US/08787335
Patent No. 5981834
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
APPLICANT: Umbeck, Paul F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line;
MOLECULE TYPE: cl
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-OCT-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 04-OCT-1988
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STRAIN: Coker 312
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                 682 GTCGGTGGCGCAGGCGACGTCCACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATAACCGTGACAGCCACCTTTTGTCCACCTAACTATGCTTTATCTAGTGACAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCAATACCGAGCTGGTATCGTCCCCGTCTCCCTTTCGTAGGGTACCATGTATGAAGAAA
                                                                                                                                                                GCTGGTTGGCAATTCGGACAAACTTTTGAAGGAGGCCAGTTTTAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAAC
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                                                                                                                                                                                                  TCCAATTGGCAATTTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCA 910
                                                                                                                                                                                                                                                                        CTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCACTGCCTATAATCTCGTTCCT
                                                                                                                                                                                                                                                                                                           CCTATGTCCAGAAATTGGGGCCAAAACTGGCAGAGCAATGCTTACCTTAACGGACAAAGC
                                                                                                                                                                                                                                                                                                                                                                               GTGGGAGGGGCAGGGGATATAACGTCAGTGTCCATCAAGGGTTCCAGAACAGGATGGCTA
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72.5%;
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Pred. No. 4.5e-70;
0; Mismatches 129;
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CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,797
FILING DATE:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-88
FILING DATE: 04-OCT-88
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 1122990245
REFERENCE/DOCKET NUMBER: 1122900245
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Matches 340;
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LIBRARY: CKFB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brill, Winston J.
TITLE OF INVENTION: GENETICALY ENGINEERED COTTON PLANTS
TITLE OF INVENTION: FOR ALTERED FIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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HYPOTHETICAL: no
ANTI-SENSE: no
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: 10 TISSUE TYPE: fiber cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles and Brady
STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/787,335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                           181
                                                                                                                                                                                              562
241
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                                                                                                                                                                                                                                                                        442 ATTAGGGTCACTGCCACCAACTTTTGCCCCTCCTAACTTTGCTCTCCCTAACAACAATGGT 501
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WISCONSIN
                                                                                                                                                         GCAGAATATCGAGCTGGAATCGTCCCTGTTATGTTCAGAAGGGTGTCATGTGTGAAGAAA
GTGGGAGGGGCAGGGGATATAACGTCAGTGTCCATCAAGGGTTCCAGAACAGGATGGCTA
                                  GTCGGTGGCGAGGCGACGTCCACTCTGTGTCGATAAAGGGGGTCTCGAACTGGATGGCAA 741
                                                                           GGAGGCATCAGGTACACCATGAATGGACATTCGTACTTCAACATGGTGTTGATAACGAAC
                                                                                              GGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAAC
                                                                                                                                                                                            GCTCAATACCGAGCTGGTATCGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAA 621
                                                                                                                                                                                                                                     GGGTGGTGCAATCCCCCACGAGAACACTTTGATTTGGCCGAACCGGCATTCTTGCGGATA 120
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72.5%;
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                                                                                                                                                                                                                                                                                                                                                                                             0; .Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 262.6; DB 2;
Pred. No. 4.5e-70;
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US-07-885-970A-26
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                                                   Matches 458;
                                                                         Query Match
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                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/253
RILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,970
                                                                                                                                                                                                                                                                                         TELEFAX: (608) 251-51
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                                     STRAIN: Sea IS IMMEDIATE SOURCE:
                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: GOS
                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21-NOV-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19920518
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICANT: John, I
                                                                                                      LIBRARY: EMU-
                                                               Local Similarity
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                    TYPE: NUCLEIC
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               TGGCACCATGGGTGGAGCTTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAA 338
TGTTTCTATAGGGGGAGCTTGTGGTATGGAAACCTGTACAGTCAAGGGTATGGAACGAG 1035
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P.O. Box 2113,
                                                                                                                                                                                                                                                                 2415 base pairs
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                                                            25.9%;
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First
                                                 0
                                               Score 256.6; DB 1;
Pred. No. 5.9e-68;
D; Mismatches 174;
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                                               Indels
                                                                      Length
                                                                        2415;
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                                               77;
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                                               Gaps
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US-08-298-687A-26
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                                   FILING DATE:
                                                                                                                                                COUNTRY:
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Sequence 26, Application US/08298687A
Patent No. 5521078
GEMERAL INPORMATION:
APPLICANT: John, Maliyakal E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                            SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     862 TCCAATTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCA 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Nicholas J.
P.O. Box 2113,
                                                                                                                                                                                                                                                                                                                                                             USA
   US 07/617,239
                                                                                                                     US/08/298,687A
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First
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US-08-298-687A-26
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REGISTRATION NUMBER: 27,386
TELEPHONE: (608) 283-2478
TELEPHONE: (608) 283-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2415 base pairs
TYPE: nucleic acid
GTPANEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-OCT-1988 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: EMBI
CLONE: SIB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Gossypium barbadense
STRAIN: Sea Island
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CTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCACTGCCTATAATCTCGTTCCT
                                                                                                                                                                                                                                                           GGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAAC
                                                                                                    TCCATGTCTAGAAATTGGGGCCAAAACTGGCCAAAGCAACTATCTCAATGGCCAAGGC
                                                                                                                                               GTGGGAGGGCAGGGGATATAACGTCAGTGTCCATCAAGTGTTCCAAAAACAGGATGGCTA 1515
                                                                                                                                                                           GTCGGTGGCGCAGGCGACGTCCACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAA
                                                                                                                                                                                                                                 GGAGGCATCAGGTACACCATGAATGGACATTCGTACTTCAACATGGTGTTGATAACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                  GAATCGTCCCTGTTATGTTCAGAAGGTGGTGAATAAAACTCAATTCAAATCATCACACTC 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATCGTCCCCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTCCAACACTTCGACATGGCTGAGCCTGCCTTCCAAATCGCTCAATACCGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAACTTTTGCCCTCCAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCTC
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                                                                                                                                                                                                                                                                                                                                                       TCTCCTTTCGTAGGGTACCATGTATGAAGAAA
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                                                                                                                                                                                              ; CLONE: SIB12
US-08-298-829-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08298829 Patent No. 5620882
                                                                                                                Query Match 25.9%;
Best Local Similarity 64.6%;
Matches 458; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: UFILING DATE: 18-MAY-1PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatil OPERATING SYSTEM: PC-DOS. SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  STRAIN: Sea Island
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27,386 TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 283-2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/253,243 FILING DATE: 04-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                    LIBRARY:
                                                                                                                                                                                                                                                                                          ORGANISM: Gossypium
                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2415 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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  339 CACGGTGGCGCTGAGCACTGCGCTATTTAACAATGGATTAAGTTGTGGTGC-TTGCTTCG 397
                                        976 TGTTTCTATAGGGGGAGCTTGTGGTTATGGAAACCTGTACAGTCAAGGGTATGGAACGAG 1035
                                                                      279 TGGCACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAA 338
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                Score 256.6; DB 1;
Pred. No. 5.9e-68;
0; Mismatches 174;
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Plaza
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                                                                                                                                                      Length 2415;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application Patent No. 5929303
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-845-539-1
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
       ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,
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US-09-362-642-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                            Sequence 1, Application Patent No. 6350935
                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 9.
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297 408 237

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Expansin Genes

Indels Length

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Sequence 3, Application:

Patent No. 5929303

Printle OF INVENTION: Expansin Genes to (
NUMBER OF SEQUENCES: 8
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CORRESSPONDENCE ADDRESS:
Townsend and Townsend and
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CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 702
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Best Local (
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NAME/KEY: CDS
LOCATION: (28)..(702)
OTHER INFORMATION: tomato expansin
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ORGANISM: Lycopersicon esculentum
STREET:
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Pred. No. 9.8e-67;
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Best Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR.1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OTHER INFORMATION:
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ilarity 69.4%;
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Pred. No. 3.9e-64;
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Search completed: December 18, 2003, 22:33:40 Job time : 91 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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C. sativus DNA enc
Cucumber expansin-
C. sativus DNA enc
Pear expansin 2 (E
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                              Description
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ABA97161
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                                                                                                                                                                                                                                                                                                                                                                                               C. sativus DNA encoding S1 expansin homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA97161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA97161 standard; DNA; 684 BP.
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56.6 25.9 2 56.6 25.9 2	மைய	62.6 26.5	62.6 26.5	270 27.2	.6 29.0	98.6 30.1	01.2 30.4 98 8 30 1	01.2 30.4	01.8 30.4	13.4 31.6	13.6 31.6	16.6 31.9	21.8 32.4	8.2 34.1	8.4 34.1	1.6 34.4	6 34.4	35.4	354 35.7	60.4 36.3	60.4 36.3	60.6 36.	61.8 36.5	6.8 3	77.8 38.1	77.8 38.1
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## ALIGNMENTS

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CDS
                                                             05-JUL-2000; 2000DE-1032630
                                                                                               22-NOV-2001.
                                                                                                                              DE10032630-A1
                                                                                                                                                                                                                                                                              Cucumis sativus.
(FARB ) BAYER AG
                             16-MAY-2000; 2000DE-1023561
                                                                                                                                                           product= "S1 extensin homologue"
/note= "No start codon given"
                                                                                                                                                                                            partial
                                                                                                                                                                                                                                               Location/Qualifiers
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This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of extensins possible. This sequence encodes the Cucumis sativus (cucumber) SI extensin homologue described in Sequence 684 BP; 163 A; 179 C; 164 G; 178 T; 0 other; Claim 2; Page 11-14; 22pp; German. Vector encoding an expansin, useful in treatment of cellulosic materials for paper recycling, providing large-scale production -Berendes F, 2002-155755/21. AAG80768. Vogt U, Gouloudis C; TO TOD: TO THE HOWAS FOT WEST FOR

Query Match
Best Local Similarity
Matches 684; Conserv 69.0%; Score 684; DB 24; Length 684; 100.0%; Pred. No. 2e-184;

밁 Ś 밁 Ś 밁 Ş 맑 Ś 밁 Ś В ş 301 523 241 463 181 403 121 343 283 223 61 CAACACTTCGACATGGCTGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGGTATC ACTTGTACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAAC 240 ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACG ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACG. 342 GACTACGGTGGCTGGCAGAGCGGCCACCTTTTATGGTGGTGGTGACGCATCTGGC GACTACGGTGGCTGGCAGAGCGGCCACGCTTTTATGGTGGTGGTGACGCATCTGGC TTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAGGTGGATGGTGCAACCCTCCTCTC 522 ACTTGTACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAAC CAACACTTCGACATGGCTGAGCCTGCCTTCCAAATCGCTCAATACCGAGCTGGTATC TTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCCTCTC Conservative <u>,</u> Mismatches <u>,</u> Indels 0, 180 120 582 300 402 60 360 462 0

## 밁 661

Expansin-29; plant cell wall; cellulose; paper recycling;
polysaccharide; cucumber; ss. 25-MAR-2003 08-JUL-1996 06-DEC-1995; 04-APR-1996 Cucumis sativus var. Burpee Pickler Cucumber expansin-29 cDNA. AAT13320 (updated)
(first entry) 95AU-0040262 DNA; ВP

12-MAY-1993; 12-MAY-1995; 12-MAY-1994; 93US-0060944. 95US-0440517. 94AU-0068320.

(PENN-) PENN , 5 STATE RES FOUND McQueen-Mason

WPI; 1996-201150/21

Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling

60pp; English.

a member of a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. It was obtd, by PCR amplification of cucumber seedling cDNA using primers based on isolated peptide fragments of the protein. The gene can be expressed in bacterial or other systems for use in recombinant expansin prodn. Expression of the gene in transgenic plants may allow alteration of plant growth characteristics, while expression in plant tissue cultures may allow improved prodn. Of useful chemicals. A cDNA clone (AAT13320) codes for cucumber expansin-29 (AAR94527), (Updated on 25-MAR-2003 to correct PF field.)

Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;

Ś 밁 S 밁 Ś Query Match
Best Local Similarity
Matches 681; Conserv 343 GACTACGGTGGCTGGCAGAGCGGCCACCCTTTTATGGTGGTGGTGACGCATCTGGC ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACG GACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTTATGGTGGTGACGCATCTGGC **ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACG** ilarity 100.0%; Conservative ( 68.6%; 0; Score 681; DB 17; 1; Pred. No. 1.4e-183; Mismatches 0 Indels 0 Gaps 402 342 60 282 120

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822 540

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882 600 CACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGC 762

AATGGCCACTCATACTTCAACCTCGTTTTGATCACAAACGTCGGTGGCGCAGGCGACGTC

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AATGGCCACTCATACTTCAACCTCGTTTTGATCACAAACGTCGGTGGCGCGAGGCGACGTC

GTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTTACAATC

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ACCTATGAAGGCCCTCAATTCTAA 906

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P-PSDB; AAG80769.
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Ś 밁 Ş 밁 S 밁 S

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Vector encoding an expansin, useful in the materials for paper recycling, providing
                                                                                     Page 14-16; 22pp; German
                                                                                                  treatment of cellulosic ng large-scale production
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This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of extensins possible. This sequence encodes the Cucumis sativus (cucumber) extensin, csexpla, described in

681 B₽; 161 A; 178 Ç 164 <u>ი</u> 178 T; other;

Length

681;

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Best Local Similarity 99.6%;
Matches 678; Conservative
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AD032964

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                             Query Match
Best Local Sim
Matches 553;
                                                                                                                                                                                     The present invention relates to novel genes which encode cell wall hydrolass such as beta-galactosidase (beta-Gal), pectin methylesterase (PME), polygalacturonase (PG) and cell wall proteins such as expansin! (Expl) and expansin2 (Exp2) proteins from pear fruit. The nucleic acids are useful for regulating fruit ripening and for suppressing endogenous beta-Gal, PME, PG, Expl and Exp2 genes in any fruit or other plant organs, thus modifying the structure of the cell walls of the fruit or plant and providing for ripe yet firm fruit and vegetables. The genes may be used to screen a cDNA library or a genomic library from any species, to inhibit or enhance gene expression or to produce transgenic plants. The present sequence is a cDNA encoding pear expansin 2 protein.
                                                                                                                                         Sequence 1144 BP; 325 A; 258 C; 242 G; 319 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New beta-galactosidase, pectin methylesterase, polygalacturonase, expansin1, and expansin2 proteins and nucleic acids, useful for regulating fruit ripening or creating transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matias Fonseca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 38-39; 45pp; English.
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beta-Gal; polygalacturonase; PG; expansin1; Exp1; expansin2; Exp2;
ripening; gene expression; transgenic plant; transgenic; enzyme;
                                                       Similarity
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Pred. No. 1e-
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t= (pos:353..361, aa:Gln-Pro)
t= (pos:413..421, aa:Gln-Pro)
t= (pos:479..487, aa:Gly-Ala)
t= (pos:767..775, aa:Gly-Ala)
t= (pos:773..781, aa:Arg-Asn)
t= (pos:66..814, aa:Trp-Leu)
t= (pos:66..814, aa:Trp-Leu)
t= (pos:66..814, aa:Trp-Leu)
t= (pos:66..814, aa:Trp-Leu)
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Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
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99US-0130449. 99US-0130077. 99US-0130077. 99US-0130077. 99US-0130081. 99US-0132487. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0134218. 99US-0136323. 99US-0136323. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139459. 99US-0139459. 99US-0139459. 99US-0139459. 99US-0139459. 99US-0139461. 99US-0140823. 99US-0141842. 99US-0142390. 99US-0142390. 99US-0142390. 99US-0142390.	2000EP-0301439.  99US-0121825. 99US-0123180. 99US-0125788. 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128234.
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                                                      AAAGGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACA
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                                                                                                                                                                                                        GEAGGTTGGTGCAATCCTCCTCTTCAGCATTTCGACCTCGCCGAGCCAGCTTTTCTTCAG
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                            AAAGGAGGAATAAGGTTTACGATCAACGGACACTCATACTTCAACCTCGTTCTGATCTCC
                                                                                                                 ATCGCTCAGTATCGTGCCGGCATTGTTCCTGTCTCTTTCCGAAGAGTACCATGTATGAAG
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                       Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
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thaliana; plant; gene; stress; transgenic;
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24-AUG-2000;
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   Claim
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                                           Identifying a and producing
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                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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SYNGENTA PARTICIPATIONS
SEQ ID NO 1088; 577pp + Sequence Listing; English
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; 2001US-264647P.
; 2001US-300111P.
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                                           stress condition to which a plant cell has been exposed plants with increased tolerance to these abiotic stresse
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CC The invention relates to identifying a stress condition to which a plant CC cell has been exposed, comprising:

C( a) contacting nucleic acid representative of expressed polynucleotides coin the plant cell with an array or probes representative of the plant CC in the plant cell with an array or probes representative of the plant CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell CC characteristic of a stress response. The method is useful in the producing plants contaction of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that cell contaction of the invention.

CC Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 762 BP; 202 A; 196 C; 184 G; 180 T; 0 other;

Local Similarity

520;

0;

Score 394.2; DB 24; Pred. No. 6.9e-102; 0; Mismatches 188;

Indels Length

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Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; 89.
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                                                                                                                                                                                                                                                                                       CGTCCACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTG
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                  DNA;
                                                            entry)
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18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999;

13-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 21-0CT-1999 21-0CT-1999

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Best Local Sim
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16-SEP 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                          CAACTTTTGCCCTAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCC
                                                                                                                                                                                                                  AATGACTTGTACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCAC
  TATCGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTTAC
                                                              TCTCCAACACTTCGACATGGCTGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGG
                                                                                                                ANACTTCTGCCCGCCAAATAACGCGTTAGCGAACAATAATGGCGGTTGGTGTAATCCTCC
                                                                                                                                                                                              GATAAGATGTGAAAACGATGGTAAATGGTGTTTACCTGGCTCAATCGTTGTAACCGCTAC
                                                                                                                                                                                                                                                                        CACGGCGCTCTAAGCACAGCTCTCTTCAACAATGGACTTAGCTGTGGTTCTTTGCTTTGA
                                                                                                                                                                                                                                                                                                            CGGCACAATGGGTGCTTGTGGATATGGTAATCTATATAGCCAAGGCTACGGGACGAG
                                      TCTTGAACACTTTGACCTTGCTCAGCCTGTTTTTCAACGCATTGCTCAGTACAGAGCTGG
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ilarity 72.0%;
Conservative
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99US-0154018
99US-0154039
99US-0155436
99US-015659
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25-FEB-1999

05-MAR 1999

09-MAR 1999

23-MAR-1999

25-MAR-1999

06-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

06-MAY-1999

06-MAY-1999

11-MAY-1999

11-MAY-1999

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99US-0121825.
99US-012548.
99US-0125788.
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Query Match 38.1
Best Local Similarity 72.0
Matches 493; Conservative
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29-OCT-1999;
Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
                                  Arabidopsis
                                                        17-OCT-2000
                                                                                                    AAC40035 standard; DNA; 1236
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                                                                                                                                                                                                                                                               GGGCCAAAACTGGCAAAGCAACAACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCAC
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                                                                                                                                                                                                                                                                                                                                            GATAAACGGCCACTCATACTTCAACCTTGTGCTGATCACAAACGTCGGTGGTGCCGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                       TATCGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGGTTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACTTTTGCCCTCAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCC
                                                                                                                                                           CCAGACTTTTGCCGGTGGACAGTTC
                                                                                                                                                                        CCAAACCTATGAAGGCCCTCAATTC
                                                                                                                                                                                                       CACCAGCGACGGCCCACAGTTGTCTCCTTCAACGCCGCTCCTGCCGGCTGGTCTTATGG
                                                                                                                                                                                                                                                   GGGGCAAAATTGGCAAAGCAACTCTTACCTCAACGGTCAAGCACTTTCCTTTAAGGTCAC
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                                   thaliana
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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21-MAY 1999;
25-MAY 1999;
27-MAY 1999;
27-MAY 1999;
28-MAY 1999;
03-JUN 1999;
04-JUN 1999;
04-JUN 1999;
07-JUN 1999;
10-JUN 1999;
10-JUN 1999;
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05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

26-APR-1999

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16-APR-1999

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 9908-0121825.
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Best Local Similarity 71.
Matches 493; Conservative
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                                                                                                                                                 CTCTTGAACACTTTGACCTTGCTCAGCCTGTTTTTCAACGCATTGCTCAGTACAGAGCTG
          CTCTCCAACACTTCGACATGGCTGAGCCTGCCTTCCAAATCGCTCAATACCGAGCTG
                                  AAATGACTTGTACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCA
                                                                                                                                                                                        CGCTGACTACGGTGGCTGGCAGACGGCCACGCCACCTTTTATGGTGGTGGTGACGCATC
                                                                        AGATAAGATGTGAAAACGATGGTAAATGGTGTTTACCTGGCTCAATCGTTGTAACCGCTA
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Pred. No. 5.4e-94;
0; Mismatches 192;
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28-JUN-1999
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01-JUL-1999
01-JUL

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S-014184 S-0142055 S-0142055 S-014205 S-0144205 S-014406 S-014508 S-0

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This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N. tabacum DNA
                                                                                                                                                                                                                                                                                                                                                  Vector encoding an expansin, useful in treatment of cellulosic materials for paper recycling, providing large-scale production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum.
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                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                              Page 19-21; 22pp; German.
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                       GAAGGCCCTCAATTCTA
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                                                                                                                                                                  GTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGCCAAAAC
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                                                  GGCCGCAGTTTGATTTCCTACAATGTTGCACCTGCTCATTGGTCTTTTGGACAGACTTAT
                                                                         GGTCGCACTCTCACTGCCTATAATCTCGTTCCTTCCAATTGGCCAATTTGGCCAAACCTAT
                                                                                                   TGGCAAAACAACAATTATCTTAATGGCCAAACGCTCTCATTTAAGGTTACTACAGGTGAT
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26-JAN-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
                                                                                                                                                                                                                                                                                                                                                                                          of an Arabidopsis thaliana stress regulated gene (ABZ12196 in methods of the invention.

Note: The sequence data for this patent is not represented specification but is based on sequence information supplied
                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                CAAAACGATGGAAAATGGTGTCTTCCTGGCTCAATTGTCGTCACAGCCACAAACTTTTGC
                                                                                                                                                     ACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAACTTTTGC
                                                                                                                                                                                                                         GGAGGTGCTTGTGGATACGGAAACCTATATAGCCAAGGCTATGGAACCAACACGCCGGCG
                                                                                                                                                                                                                                                                   GGAGGTTGGGTCAACGCACACGCCACATTCTACGGTGGTGATGCTTCCGGCACAATG
GTCGCTTACCGAAGAGTGCCGTGCGTGAGAAGAGGAGGAATAAGGTTTACGATAAACGGA
                    TTCGACATGGCTGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGGTATCGTCCCC
                                                                                     CCTCCTAACAACGCCTTACCGAACAACGCAGGAGGTTGGTGTAACCCTCCTCAGCAGCAT
                                                                                                          CCTCCTAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCCTCCCAACAC
                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-227866P.
; 2001US-264647P.
; 2001US-300111P.
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PARTICIPATIONS
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71.1%;
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Pred. No. 2.5e-92;
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                               The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used Note: The sequence data for this parent.
         Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                            24-AUG-2000; 2000US-227866P.
26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
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Best Local Simi
Matches 496;
                          Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Pred. No. 2.9e-92;
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US-09-896-301-1

Sequence 1, Application US/09896301 Patent No. US20020103355A1

## ALIGNMENTS

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TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/IC114US3
CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR FILING DATE: 1994-05-12
PRIOR FILING DATE: 1994-05-12
PRIOR FILING DATE: 1994-05-12
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                         Matches 681; Conservative
                                                                  Query Match
Best Local Similarity 100.0%;
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
                                                                                                                                                                                                      LENOTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
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223 GACTACGGTGGCTGGCAGAGCGGCCACCTTTTATGGTGGTGGTGACGCATCTGGC 282
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; Pred. No. :
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILLE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1088
LENGTH: 762
TYPE: DNA
OFFICANTION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1088, Application Patent No. US20020160378A1
ORGANISM: Arabidopsis thaliana
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                                                                                                 Sequence 3, Application US/10150559

Publication No. US20030221218A1

GENERAL INFORMATION:

APPLICANT: Wilkins, Thea A.

APPLICANT: The Regents of the University of

TITLE OF INVENTION: Bioengineering Cotton Fil

FILE REFERENCE: 023070-116500US

CURRENT APPLICATION UNMBER: US/10/150,559

CURRENT FILING DATE: 2002-05-17

NUMBER OF SEQ ID NOS: 23
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           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1153
TYPE: DNA
ORGANISM: Gossypium hirsutum
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Best Local Similarity
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Pred. No. 1.8e-104;
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Sequence 8, Application US/10409701
Publication No. US20030221224A1
GENERAL INFORMATION:
APPLICANT: Zinselmeier, Chris
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Holentjaris, Timothy G.
APPLICANT: Holentjaris, Timothy G.
FILE REFERENCE: 1421
CURRENT APPLICATION NUMBER: US/10/409,701
CURRENT APPLICATION NUMBER: US/0370,796
PRIOR FILING DATE: 2003-04-08
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 26
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 759
                                                                                                                                                                                                                                                         RESULT 4
US-10-409-701-8
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Pred. No. 5.1e-102;
0; Mismatches 203;
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Sequence 91, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Tong
APPLICANT: Youn
APPLICANT: Youn
APPLICANT: Shu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A
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US-09-938-842A-91
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Best Local Sim
Matches 492;
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ORGANISM: Zea
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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RESULT 6
US-09-938-842A-1069
US-09-938-842A-1069; Sequence 1069, Application US/09938842A; Patent No. US/0020160378A1; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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Best Local Simi
Matches 477;
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LENGTH: 753
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ORGANISM: Arabidopsis thaliana
-09-938-842A-91
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                                                                                                                           ACAGGTGCGCA
                                                                                                                                                       GAAGGCCCTCA 899
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Pred. No. 1.2e-94;
0; Mismatches 194;
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APPLICANT: MANG, XUN
APPLICANT: Zhu, TONG
APPLICANT: Zhu, TONG
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
SEQ ID NO 1069
LENGTH: 747
TYDE: DNA
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Best Local :
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TCTCTAACAACATTGCTCCAGCTAGTTGGTCCTTTGGACAAACCTTCACCGGCCGTCAAT
                                CTGCCTATAATCTCGTTCCTTCCAATTGGCCAATTTGGCCAAACCTATGAAGGCCCTCAAT
                                                                                          ACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCA
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Pred. No. 1.4e-94;
0; Mismatches 226;
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
ITITE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRA
ITITE OF INVENTION: SAME, AND METHODS OF USE
ITITE OF INVENTION: SAME, AND METHODS OF USE
ITITE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 89
LENGTH: 774
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Best Local
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ORGANISM: Arabidopsis thaliana
-09-938-842A-89
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APPLICANT: Kreps, Joel
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Local Similarity 69.9%;
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CCAAAACTGGCAAAGCAACAACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCT 821
                                                                                                                                     CAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAACGTCGGTGGCGCAGGCGACGT 701
                                                                                                                                                                                                          CGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTTACAAT 641
                                                                                                                                                                                                                                                                                  CCAACACTTCGACATGGCCTGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGGTAT 581
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                                                                      CCACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGG 761
                                                                                                                                                                                 TGTCCCCGTCTCATACCGCAGGGTGCCATGTAGAAAGAGAGGAGGCATAAGGTTCACAAT 503
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                                  CGTGAGGGCTAGTGTGAAAGGATCACGGACTGGTTGGATGAGTTTGAGCAGAAACTGGGG
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US-09-938-842A-842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT FAPPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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APPLICANT: Kreps, Joel
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 30.4%; Local Similarity 67.0%;
                                                                        385
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                       GTCCCCGTCTTCCTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTTACAATC
                                                                                                                                                                                                                                                              ACAAACGACCCTAAATGGTGCCTTCCGGGAA-----CTATTAGGGTCACTGCCACCAAC 462
                                                                                                                                                                                                                                                                                                                         GGAGGAGCTTGTGGTTATGGTAACTTATACAGCCAAGGCTATGGTGAACACGGCGGCT 204
                                                                                                                                                                                                                                                                                                                                                                                                        GGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACGGTGGCG 348
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GTCCCCGTCTCTTTCCGCCGAGTGCCCATGCCGGAAGAGAGGAGGAATAAGGTTCACAATC
                                                                        CCTCACTTTGATCTTGCTATGCCTATGTTTCTCAAGATCGCTGAGTATCGTGCCGGAATC
                                                                                                            CAACACTTCGACATGGCTGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGGTATC 582
                                                                                                                                               GCTAGTGATCCAAAATGGTGCCATTCTGGTAGTCCTTCAATCTTCATCACTGCGACTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGGTTGGGAAACTGCTCACGCCACTTTCTACGGTGGCTCTGATGCTTCTGGAACAATG 144
                                                                                                                                                                             TTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCCTCTC 522
                                                                                                                                                                                                                                                                                                   TTAAGCACGGCTCTGTTCAACAATGGTTTTAGCTGTGGTGCTTGTTTTGAGCTCAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 301.2; DB 10;
Pred. No. 2.8e-77;
0; Mismatches 213;
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US-09-770-445-491/c
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                                                                                                                                                                              NAME/KEY: misc feature
; LOCATION: (1)...(893)
; OTHER INFORMATION: n = A,T,C
US-09-770-445-491
                                                                                                                                                                                                                                                                         SOFTWARE: FA
SEQ ID NO 491
LENGTH: 893
TYPE: DNA
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                                                                                                                      Query Match
Best Local Similarity
Matches 442; Conserv
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
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                 GGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACGGTGGCG
                                                                              GGTGGCTGGCAGAGCGGCCACCTTTTATGGTGGTGGTGACGCATCTGGCACCATG
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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                                                            GGTGGTTGGGAAACTGCTCACGCCACTTTCTACGGTGGCTCTGATGCTTCTGGAACAATG
                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis, Keith R.
Allen, Keith
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Slader, Ted
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                                                                                                                        Conservative
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                                                                                                                    Score 298.8; DB 9;
Pred. No. 1.5e-76;
0; Mismatches 216;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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US-09-878-574-3973
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                                                                                                                      ; ORGANISM: Glycine m
; OTHER INFORMATION:
US-09-878-574-3973
                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3973
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3973, Application US/09878574 Patent No. US20020110548A1 GENERAL INFORMATION:
                                                          Query Match
Best Local Similarity
Matches 321; Conserv
                                                                                                                                                                         TYPE: DNA
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              488 CTAACAACAATGGTGGATGGTGCAACCCTTCCTCCCAACACTTCGACATGGCTGAGCCTG
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CTAACAACAATGGTGGCTGGTGCAACCCTCCTTTGCAACACTTTGATCTTGCTGAGCCTG
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                                                           Score 270; DB 10;
Pred. No. 2.5e-68;
0; Mismatches 85;
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US-09-938-842A-1046
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                                                                                                                                                                                                                                                                                                                         Matches 454;
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1046
LENGTH: 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: STRESS-REGULATED GENES OF TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              899
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                                                                                                                                                                                                  CTACGGTGGCTGGCAGAGCGGCCACCTTTTATGGTGGTGGTGACGCATCTGGCAC
                                                                                                                                                                                                                                                                             TTACTCACCCTTCTCTCTTCTTCTTCTTCTTCTTTGTCTTCACCTTCGCTGA 224
                                                                                                                              CATGGGTGGAGCTTGTGGGGAATGTGATATATACAGCCAAGGGTATGGCACGAACACGGT 344
                                                                                                                                                                             TTCTGCTGGTTGGTTGCAAGCTCATGCGACCTTTTATGGCGGAAGTGATGCCTCTGGTAC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAATCTCGTTCCTTCCAATTGGCAATTTGGCCAAACCTATGAAGG 893
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       TTGT---
                                                                       AATGGGTGGAGCTTGTGGTTATGGAAACCTATACACAGACGGCTACAAGACAAACACCGC 191
                                                                                                                                                                                                                                                 TTTCTCTCTATTGGTCGCAATGATCTTCTCCACAATGTTCTTCATGAAGATCAGCTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Xun
Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAACATTGTGCCTGCTAACTGGCAATTTGGACAAACATTTGAAGG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAATGGCCAAAGCCTCTCTTTTCAGGTCACTACAAGTGATGGCAGGACTCTCACTAGCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCACTGCCT 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGTGTGAAGAAAGGAGGGATCAGGTTCACCATCAATGGTCACTCTTACTTCAACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATGTATGAAGAAAGGTGGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTCTTGCAAATTGCTCAATACAAAGCTGGAATTGTTCCAGTTTCCTTCAGAAGAGTCT 122
                                      GGCGTTAAGCACGGCCCTGTTCAACGACGGCAAGTCATGCGGTGGATGTTACCAAATCTT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTCCTTCAAATCGCTCAATACCGAGCTGGTATCGTCCCCGTCTCCTTTCGTAGGGTAC
                                                                                                                                                                                                                                                                                                                         Conservative
   --ACAAACGACCCTAAATGGTGCCTTCCGGG---AACTATTAGGGTCACTGC 455
                                                                                                                                                                                                                                                                                                                                       25.3%;
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                       Score 251.2; DB 10;
Pred. No. 1.1e-62;
0; Mismatches 268;
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                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                          768;
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                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                       APPLICANT: Byrum, Joseph R.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 62
LENGTH: 391
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(391)
OTHER INFORMATION: Clone ID: LIB3028-056-Q1-1
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US-09-878-574-62
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                                                                                                                                                                                                US-09-878-574-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US2002011
GENERAL INFORMATION:
                                                                                                                            Matches
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                                                                                                                                           Query Match
Best Local
559 ATCGCTCAATACCGAGCTGGTATCGTCCCCGTCTCCTTTCGTAGGGGTACCATGTATGAAG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                873
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                                                                                                                            302;
                                                                                                                                           Similarity
                                                      GTTTGGTCAGAGCT 745
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                                                                                                                        Conservative
                                                                                                                                           25.3%;
77.8%;
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LIB3028-056-Q1-B1-E10
                                                                                                                        0;
                                                                                                                        Score 251; DB 10;
Pred. No. 8.6e-63;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Other Molecules Associated with
                                                                                                                            96;
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                                                                                                                          Indels
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Gaps

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60

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APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
ITITLE OF INVENTION: Expressed Sequences of Arabidopsis
ITITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 430
LENGTH: 366
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                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis
US-09-770-791-430
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US-09-770-791-430
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                                                                                                                     Query Match
Best Local Similarity
Matches 238; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                288
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                    GGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCACTGCCTATAATCTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATCCATGTCTAGAAATTGGGGCCAAAAACTGGCAAAGCAACAACTATCTCAATGGCCAA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGTGGCTGGAGCTGGTGATGTGAATTCAGTGTCCATTAAAGGGTCCAAAACTGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGTCGGTGGCGCAGGCGACGTCCACTCTGTGTGGATAAAGGGGTCTCGAACTGGATGG
                                                                            CCTTCCAATTGGCCAATTTGGCCAAACCT 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGGTGGAGTGAGGTTTACAATCAATGGCCACTCATACTTCAACCTTCGTTTTGATCACA 678
   GGGCGGCGTGTGGGTACGGGAACTTGTACAGCCAAGGATACGGTGTGAACACGGCGGC
                                                             CGGACCGTGGCAGAATGCACACGCCACTTTCTACGGTGGCAGTGACGCCTCCGGCACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Garcia, Carlos A.
Kricker, Maja
Slader, Ted
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Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                   Davis, Keith R.
Allen, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page, Amy
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abraham V.
                                                                                                                                  17.18;
71.78;
                                                                                                                                                                                                thaliana
                                                                                                                     0;
                                                                                                                     Score 169.2; DB 9;
Pred. No. 6.6e-39;
0; Mismatches 88;
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Sequence 1206, Application US/0
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
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APPLICANT: Byrum, Joseph R.
APPLICANT: Tha Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules :
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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SEQ ID NO 3468
LENGTH: 373
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OTHER INFORMATION: Clone ID:
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Pred. No. 5.3e-33;
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US/09878574

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; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1206
; SEQ ID NO 1206
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-040-Q1-B1-G6
Search completed: December 18, 2003, 23:35:20 Job time : 368 secs
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Riverside, CA, 92521-0124, US
Tel: 9097874137
Fax: 9097874437
                                                                               Unpublished
                 Email: mikeal
        primer: T3
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CD574577 880 bp mRNA linear EST 12-JUN-2003 UCRPT01\_06\_G11\_T3 Poncirus trifoliata CTV-challenged cDNA library -UCR Poncirus trifoliata cDNA clone UCRPT01\_06\_G11, mRNA sequence. CD574577 •

ALIGNMENTS

CD574577.1 GI:31670479

Poncirus trifoliata
Poncirus trifoliata
Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatcophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Poncirus.

1 (bases 1 to 880)
Roose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D.,
Wanamaker, S., Choi, Y., and Kingan, T.
Development of EST Resources and New Genetic Markers for California
Citrus - Poncirus trifoliata CTV-challenged phloem - UCR

Contact: Mikeal Roose USA Sciences,

University of California

Location/Qualifiers .roose@ucr.edu

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Core Instrumentation Pacility, (Choi, Kingan).

Chromatogram files were transmitted to UC Riverside (by Choi), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region.

Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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library - UCR"
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/lab_host="E. coli TJC121"
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/clone="UCRPT01_06_G11"
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/cultivar="Pomeroy
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BG581975
BG581975.1 GI
                                                                                                                                                                                                                                                                                                                                  Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M33038e TIGR
MTCDB60TK More information is available at:
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Agronomy and Plant Genetics University of Minnesota 411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715 Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
jeurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Ge, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, CESTs from one month old nitrogen-fixing root nodules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG581975 798 bp mRNA linear EST EST483712 GVN Medicago truncatula cDNA clone pGVN-66I24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   truncatula, 2001
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/clome_lib="GVN"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
                                                                                                             /db_xref="taxon:3080"
/clone="pGVN-66124"
/tissue trype="N2-fixing root nodules"
/tessue="effective root nodules harvested opost inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                     organism="Medicago truncatula"
/mol_type="mRNA"
                                                                                                                                                                                                                                                cultivar="genotype"
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http://www.medicago.org
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RESULT 3
CD575807
LOCUS
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ORIGIN
                                                                          KEYWORDS
                                                                                               VERSION
                                                                                                                ACCESSION
                                                                                                                                                   DEFINITION
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Best Local
                                           ORGANISM
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                                                                       UCRPT01 01ae06 g3 Poncirus trifoliata CTV-challenged cDNA library AGI Poncirus trifoliata CTV-challenged cDNA library CD575807
CD575807
CD575807.1 GI:31671709
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Poncirus trifoliata
Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."

a 173 c 175 g 229 t
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77.1%;
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Pred. No. 1.4e-58;
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CDNA library -
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Roose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D., Wanamaker, S., Collura, K., Feuerbacher, O., Kim, H.R., Kudrna, R. and Yu, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Botany & Plant Sciences, Riverside, CA, 92521-0124, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 9097874137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mikeal.roose@ucr.edu
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Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was purified, a CDNA library was made, and 0.5 million primary lambda cDNA library was made, and 0.5 million primary lambda cDNA library was made, and 0.5 million primary lambda cDNA plasmid DNA purified, cDNA clones were in vivo excised to give a population of palsmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Peuerbacher, Kim, Kudrna, Wing, Yu).

Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to cenBank."
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/lab_host="E. coli TJC121"
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cultivar="Pomeroy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB291406 B09 bp mRNA linear EST 28-FEB-2003 UCRCS01_02dd11_g1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02dd11, mRNA
                                                                                                                                                          Department of Botany & Plant Sciences, Riverside, CA, 92521-0124
Tel: 9097873318
                                                                                                                                                                                                                                                                Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kudrna, D., Wanamaker, S., Wing, R. and Yu, Y.
Development of EST Resources and New Genetic Markers
                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core ex; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 809)
                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
CB291406
CB291406.1 GI:28616863
                                                                                                                                                                                                             Unpublished
Contact: Timothy Close
                                                                                                                                                                                                                                                                                                                                                                                        Citrus sinensis
                                                                                                                         Email: timothy.close@ucr.edu
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                                                                                                       primer:
                                                                                                                                            9097874437
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Washington Navel"
/db_xref="taxon:2711"
                                                                                       Location/Qualifiers
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during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, DNA sequences determined bi-directionally using an ABIS50 at the Arizona Genomics Institute, University of Arizona (Collura Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mature fruit was harvested at mid-day in January 2002
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/lab_host="E. coli TJC121"
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Query Match Best Local Similarity 162 AAGTGGCCATGCAACTTTCTATGGCGGGGGTGATGCTTCCGGCACAATGGGTGGTGCTTG 536; GCTATTTAACAATGGATTAAGTTGTGGTGCTTGCTTCGAAATGACTTGTACAAACGACCC TGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACGGTGGCGCTGAGCACTGC GAGCGGCCACCTTTTATGGTGGTGGTGACGCATCTGGCACCATGGGTGGACCTTG CAACCTCGTTTTGATCACAAACGTCGGTGGCGCAGGCGACGTCCACTCTGTGTCGATAAA 719 **AAGGATCCCGTGTGCGAAGAAAGGAGGAATAAGGTTTACCGTCAATGGACACTCATACTT** TAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAACTTTTGCCCCTCCTAACTT TCTCTTTCTTCCTTTCTTCTTTGTCTTCACCTTCGCTGACTA----CGGTGGCTGGCA TGAGCCCGCTTTCTTGCAAATTGCCCAATACCGCGCGGTATCGTCCCAATTTCCTTCAG TGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGGTATCGTCCCCGTCTCCCTTTCG TGCCCTGTCTAACGACAACGGCGGTTGGTGCAATCCTCCCCTCCAGCACTTTGACATGGC TGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCCTCCTCCCAACACTTCGACATGGC CAAGTGGTGCCTCCCCGGCTCCATCATTGTCACCGCCACCAACTTCTGCCCCACCTAACCT TCTATTCAACAATGGCCTAAGCTGTGGTTCATGCTATGAAATGAAATGTGAAAATGACCC TGGGTATGGCAATTTGTACAGCCAAGGCTATGGGACTAACACTGCATCACTCAGTACCGC Conservative 42.6%; 75.8%; <u>.</u> Score 422.2; DB 1 Pred. No. 1.5e-56; Mismatches 168; DB 14; Indels Length <u>ن</u> Gaps 161 659 239 581 521 599 461 539 401 479 341 419 281 359 221 299

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CB293003
CB293003.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Botany & Plant Sciences, Riverside, CA, 92521-0124
Tel: 9097873318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R., Kudrna, D., Wanamaker, S., Wing, R. and Yu, Y.
Development of EST Resources and New Genetic Markers for California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB293003 799 bp mRNA linear EST 28-FEB-2003 UCRCS01_05bf07 gl Washington Navel orange cold acclimated flavedo & UCRCS01_05bf07, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: timothy.close@ucr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Timothy Close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Citrus sinensis
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//db_xref="meaning on waver |
//db_xref="taxon:2711"
//db_xref="taxon:2711"
//tissue_type="Rind containing flavedo and albedo"
//tissue_type="Rind containing flavedo and albedo"
//dev_stage="Mature fruit"
//dev_stage="Mature fruit"
//clone_lib="Washington Navel orange cold acclimated
flavedo & albedo cDNA library"
//note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
field at University of California, Riverside Agricultural
Operations since 1983. The scion was Washington Navel
orange and the rootstock Carizzo Citrange. Tissue from
mature fruit was harvested at mid-day in January 2002
during a cold spell, when pre-dawn temperatures were
approximately -2 to 2 degree C. Approximately 2 cm median
sections of the rind were excised in the field from
several fruits, then wrapped in aluminum foil and frozen
quickly in dry ice. Total RNA was extracted using a phenol
extraction procedure described in J. Japanaese Soc. Hort.
Sci. (1996) 64:809-814. Polly(A) RNA was purified, a cONA
library was made, and 1 million primary lambda cDNA clones
were in vivo excised to give a population of pBjuescript
SK(-) phagemids. All steps to this point were performed in
the TJ Close lab at the University of California,
Riverside (Fenton). Phagemids were plated, plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Washington Navel"
/dh xref="taxon.2711"
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CACTGCCTATAATCTCGTTCCTTCCAATTGGCAATTTGGCCA 881
                                                                           CAACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCT
                                                                                                                                                         GGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGCCAAAACTGGCAAAGCAA
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                                                      TTCTTATCTTAACGGCCAAAGTCTTTCTTTCCAATTGACAGCCAGTGACGGCAGGACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeling (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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75.8%;
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RESULT 6 CB980842 LOCUS ACCESSION VERSION DEFINITION

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GACTAGCAACAATGTTGTGCCTGGAAATTGGCAATTTGGGCA 799

CB980842 838 bp mRNA linear EST 01-MAY CAB70003 IIAR A03 Cabernet Sauvignon Berry Post-Veraison - CAB Vitis vinifera cDNA clone CAB70003\_IIAR\_A03 3', mRNA sequence. CB980842 CB980842.1 GI:30304048 EST 01-MAY-2003

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SOURCE
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Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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UC Davis, Plant Pathology
One Shields Ave, Davis, CA
Tel: 530 754 6561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Douglas Cook, CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Vitaceae; Vitis.
1 (bases 1 to 838)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed sequence tags from cabernet sauvignon berries at various
GGGTCACCTGCCACCTATTTGCCCCTCCTACTTTGCTCTCCCTAACAACAATGGTGGAT
                                                                        GTGCTTGCTTCGAAATGACTTGTACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTA 445
                                                                                                                           GGTATGGCACGAACACGGTGGCGCTGAGCACTGCGCTATTTAACAATGGATTAAGTTGTG
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                                                                                                                                                                                                                               TCCAAGGCÁCAAATGGTGÁCTATGGTGGGTGGGAAGGTGGGCATGCCACATTCTATGGCG
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    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          /Clone lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"
/note="Organ: Berry; Vector: pDNR; Site 1: Sfil; Site 2:
Sfil; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8
berries. Samples were collected post-veraison from
field-grown vines during stage III of berry growth at 89
days after full bloom. Berries soluble solid concentration
ranged between 18-19 brix. Sampled vines were located at
the University of California, Davis, Experimental
Vineyard. cDNAs were made by oligo-dT priming and directi
onally cloned. 5'and 3' adaptors were used in cloning as
follows: 5'-AAGCACTGGTATCACCCAGACTGGCCATTACCGCGG-3' and
5'-ANTCTAGACGCCGACTGGTATCACCCAGACTGGCCATTACCGCCGG-3'
Size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silva, F., Iandolino, A., Lim, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CAB70003:IIaR_A03"
/sex="Hermaphrodite"
/dev_stage="Post-Veraison, 18-19 brix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cultivar="Cabernet Sauvignon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Vitis vinifera'
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:29760"
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70.5%;
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Pred. No. 5.3e-56;
0; Mismatches 234;
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338 CCGTGACTGCCACAAACTTCTGCCCTCCTAACTTGGCCTTGTCCAACACCAACGGCGGAT
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 767)
van der Hoeven, R. S., Bezzerides, J. L., Karamycheva, S. A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J. J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI932999 767 bp mRNA linear EST 18-OCT EST552888 tomato flower, 8 mm to preanthesis buds Lycopersicon esculentum cDNA clone cTOC24J22 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                            Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preanthesis
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                                                                                                                                                                                                                                                                                primer: T3
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to p
                                                                                        /db_xref="taxon:4081"
/clone="cTOC24J22"
                                                                                                                                               /mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                             organism="Lycopersicon
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RESULT 8
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CD484188.1 GI:3140545
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Amborella trichopoda
Amborella; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                              CD484188
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                                                                                                                   GI:31405456
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74.1%;
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Pred. No. 2.7e-55;
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JOURNAL
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Best Local
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The sequence provided is trimmed of vector and low c
Full sequence and original trace file are available
Genome Network website (http://pgn.cornell.edu)
Plate: atr01-4ms1 row: d column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dePamphilis,C., Soltis,D., Soltis,P., Farmerie,W., Ma,H., Tankeley,S., Leebens-Mack,J., Field,D., Buzgo,M., Kim,S., Ilut,D., Landher,L., Hu,Y., Wall,K., Albert,V., Carlson,J., Doyle,J., Frohlich,M., Miller,W., Oppenheimer,D. and Theissen,G.
Generation of ESTs from early flower buds of Amborella trichopoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 Mueller Laboratory, Department State University, University Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                   CTCTCCCTAACAACAATGGTGGATGGTGCAACCCTCCTCCCAACACTTCGACATGGCTG
                                                                                                                                            AATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAACTTTTGCCCTCCTAACTTTG
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//clone
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/dev_stage="<= 2.5mm
/lab_host="SOLR"</pre>
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/db_xref="taxon:13333"
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77.4%;
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BQ165503
BQ165503.1
                                                                                                                                                                                                                                                                                                                                     Email: kvandenb@cbs.umn.edu
TIGR sequence name: MYNAI72TK Alias Clone name:GVN-51C8
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             220 BioSci Center, 1445 Gortner Ave, Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Plant Biology University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Utterback,T., Cheung,F. and Fraser,C.M.
The Medicago truncatula 'kiloclone' set; ESTs selections and the set; ESTs selections are set; ESTs selections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST611372 KVKC Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: VandenBosch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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/clone_lib="KVKC"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; The cDNA
knoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         truncatula (barrel
                                                                                                                                                                                                                                                         organism="Medicago
/mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                  tissue_type="mixed tissues"
/dev_stage="various stages"
                                                                                                                                                                                                                db_xref="taxon:3880"
clone="pKVKC-9F12"
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Glycine max (soybean)

Glycine max (soybean)

Glycine max (soybean)

Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;

; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna Shoemaker,R., Keim,P., Vodkin,L., Kucaba,T., Martin,J., Beck,C.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
                                                                                                                                                                                                                                                             CA785153
CA785153
Gm-c1062 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1062-9317 5' similar to TR:O81133 O81133 EXPANSIN. ;, mRNA
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.resgen.com
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AGCCTGCTTTCTTGCAAATTGCTCAATACAAAGCTGGAATTGTTCCAGTTTTCCTTCAGAA
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h quality sequence stop: 409
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cubic_TVector: DBluescript II SK+; Site 1: EcoRI; Site 2: /note="vector: DBluescript II SK+; Site 1: EcoRI; Site 2: /note="vector: DBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from stem tissue of 1 month old greenhouse grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated CDNA fragments were transformed into DHIOB host cells (glbcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/mol type="mRNA"
/db xref="taxon:3847"
/clone="SOYBEAN CLONE ID: G
/tissue_type="stem tissue o
/dev_stage="l month old"
/lab_host="PH10B"
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Pred. No. 5.3e-54;
0; Mismatches 135;
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Matches 583
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CB822230

EST 3081 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus

Armeniaca cDNA clone be005k06 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unite de genetique et amelioration des Institut National de la Recherche Agron Domaine Saint-Maurice BP 94 84143 Montf Tel: 00-33-(0)4-32-72-26-68 Fax: 00-33-(0)4-32-72-26-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimplet,J., Romieu,C., Audergon,J.M., Albac
Bouchet,J.P. and Terrier,N.
High Throughput Detection of Isogenes among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; rosid; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 864)
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                                                                                             Similarity
                                     CCCACTTTTCTTCACAAACTATTTTCAAATATAAACCCATTCTTATGGCTTTTTCTTACT 169
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                                                                                                                                                                         /dev_stage="Half-Ripe stage"
/clone lib="Half-Ripe Apricot Fruit Lambda Zap II Library"
/clone lib="Half-Ripe Apricot Fruit; Site_1: Eco RI
/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco RI
; Site_2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeguie-Mbeguie D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999
a 200 g 238 t 2 others
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/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="be005k06"
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72.1%;
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                                                                           Score 404.8; DB 14;
Pred. No. 7.5e-54;
0; Mismatches 218;
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                                                                                          Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Sapindales; Rutaceae; Poncirus.

1 (bases 1 to 878)
                                                                                                                                                                                                        CD574625 878 bp mRNA linear EST 12-JUN-200 UCRPT01_0lae06 bl Poncirus trifoliata CTV-challenged cDNA library AGI Poncirus trifoliata cDNA clone UCRPT01_0lae06, mRNA sequence. CD574625.1 GI:31670527 EST.
                 Development of EST Resources and New Genetic Markers for California
Citrus - Poncirus trifoliata CTV-challenged phloem - AGI
                                                                   Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D., Wanamaker,S., Collura,K., Feuerbacher,O., Kim,H.R., Kudrna,D.,
                                                                                                                                                                                            Poncirus trifoliata
                                                       R. and Yu, Y.
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Department of Botany & Plant Sciences, University
Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
                           Similarity
                                                                                                                                               Industry Page 1.

Inches Processor: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed)
seedling of poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Polly(A) RNA was gurified, a cONA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the ML Roose lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Poncirus trifoliata CTV-challenged cDNA library - AGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UCRPT01_01ae06"
/tissue_type="Phloem"
/dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TJC121"
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/cultivar="Pomeroy
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                           40.8%;
                        Score 404.6; DB Pred. No. 8e-54;
Mismatches
                                                           DB 14;
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	EATURES	JOURNAL COMMENT	AUTHORS TITLE	ORGANISM ORGANISM	RESULT 13 9M780176 LOCUS DEFINITION ACCESSION FERSION FERSION	8 8	ያ አ	<u> </u>	8 8	8 8	8 8 8
/organism="Medicago truncatula" /mol_type="mRNA" /cultivar="genotype A17" /db xref="taxon:3880" /clone="pKV2-54C20" /tissue_type="Seedling roots" /dev stage="2 days post-inoculation with Sinorhizobium meliloti" /lab_host="E. coli strain SOLR" /clone_lib="KV2" /clone_lib="KV2" /clone_lib="KV2" /site_l: EcoRI; Site_2: /note="vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold	TIGR sequence name: www.medicago.org Seq primer: Skmod (C Location/Qu rce 1770	Unpublished Contact: VandenBosch K Department of Plant Biology University of Minnesota 220 BioSci Center, 1445 Gortner Ave, St. Paul, Tel: 612 624 2755 Fax: 612 625 1738 Email: kvandenb@cbs.umn.edu	VandenBosch, K., ,S., Utterback, ESTs from roots Sinorhizobium n		.3 BM780176 770 bp mRNA linear EST 04-MAR-2002 EST590764 KV2 Medicago truncatula cDNA clone pKV2-54C20, mRNA sequence. NM BM780176 BM780176 GI:19110266	870 GCAATTTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCATA 912 	810 TCAAGTCACTCTTAGTGATGGTCGCACTCCTCACTGCCTATAATCTCGTTCCTTCC	750 TAGAAATTGGGGCCAAAACTGGCAAAGCAACTATCTCAATGGCCAAGGCCTTTCCTT 809	690 CGCAGGCGACGTCCACTCTGTGTCCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTC 749	630 GAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAACGTCGGTGG 689	638 CAATCCTCCCCTCCAGCACTTTGACATGGCTGAGCCCGCTTTCTTGCAAATTGCCCAATA 579 570 CCGAGCTGGTATCGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGT 629
RESULT 14 BE131139 BE131139 BE131139 BE131139 BE131139 BE131139 DEFINITION L48-1090T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1090 5', mRNA sequence.  ACCESSION BE131139 VERSION BE131139 BE131139 BE131139.1 GI:8578502 KEYWORDS SOURCE ORGANISM Mesembryanthemum crystallinum (common iceplant) BUSTON Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.	Qy 840 C 840 Db 770 C 770	Qy 720 GGGTCTCGAACTGGATGCCAATCCATGTCTAGAAATTGGGGCCAAAACTGGCAAAGCAA 779	Qy 660 CAACCTCGTTTTGATCACAAACGTCGGTGGCGCAGGCGACGTCCACTCTGTGTCGATAAA 719	OF TAGGETACCATGTATGAAGAAAGGTGGAATTGACAATAAAATGGACCCATACTT 589  OF TAGGGTACCATGTATGAAGAAAGGTGGAGTTACAATGAATG	420 TANATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAACTTTTGCCCTCCTAACTT	Qy 360 GCTATTTAACAATGGATTAAGTTGTGGTGCTTGGAAATGACTTGTACAAACGACCC 419	300 TGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACGGTGGGGCTGAGCACTGC	Qy 240 GAGCGGCCACGCCACCTTTATGGTGGTGACGCATCTGGCACCATGGGTGGAGCTTG 299	Qy 183 TCTCTTCTTCTTCTTCTTCTTTGTCTTCACCTTCACCTTACGGTGGCTGGCA 239	Query Match 40.7%; Score 403.4; DB 12; Length 770; Best Local Similarity 76.7%; Pred. No. 1.3e-53; Matches 507; Conservative 0; Mismatches 151; Indels 3; Gaps 1;	packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells." BASE COUNT 214 a 164 c 169 g 223 t ORIGIN

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Seq primer: T3
High quality se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014,
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                     TTTGGCTAACAACAATGGTGGGTGGTGCAACCCTCCTCCTCAGCACTTTGACATGGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: XhoI"
a 214 c 188 g 211 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="leaf, 48 h 0.4M NaCl"
/dev stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library
, 48 hours NaCl treatment"
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/clone="L48-1090"
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/mol_type="mRNA"
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Pred. No. 1.7e-53;
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Different Gene Expression Responses in Cotton Root and Hypocotyl
tissues during infection with Fusarium Wilt Disease
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 736)
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CD486517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD486517 736 bp mRNA linear EST 04-JUN-2003 CRH3.3F02 Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH) Gossypium hirsutum cDNA clone CRH3.3F02 5' similar to expansin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive, Black Mountain, Canberra, ACT, 2601, Australia Tel: 61 2 6246 4914, 6246 5377 Fax: 61 2 6246 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector clipped sequences Bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTCGACCCACGCGTCCG): SalI
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primer: M13 reverse primer
h muality sequence stop: 736.
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NotI-oligodT primer/adapter using the manufacturers protocols (Life Technologies) and then ligated to a SalI adapter to facilitate directional cloning. The cDNA was cloned into the SalI and NotI sites of the Lambda ZIPLOX phage vector (Life Technologies). Constructed by Caitriona Dowd and Helen McFadden."
                                                                                                                                                                                        /note="Vector: Lambda ZIPLOX; Site_1: SalI; Site_2: NotI; mRNA was prepared from root and hypocotyl tissues of the cotton cultivar DeltaEMERALD. cDNA was synthesised from a
                                                                                                                                                                                                                                                                       /clone lib="Cotton Root and Hypocotyl Lambda Library (CRH)"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="DeltaEMERALD"
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/clone="CRH3.3F02"
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40.5%; Score 401.8; DB 14; Length 736; imilarity 77.3%; Pred. No. 2.4e-53; Conservative 0; Mismatches 143; Indels 0; Gaps GGTGGCTGGCAGAGGGGCCACCTTTTATGGTGGTGGTGAGGATCGAACAGGTGGCACCATG GGAAGGGTGGTGAGGAGGAGAGAGGTATGGAAGAGGGTATGGAAGAGGGTATGGAAGAGGTATGGAAGAGAGGTATGGAAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGGTATGGAAGAGAGAGAGAGAGAGAGGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	OY TGGCAAAGCAACAACTATCTCAATGGCCAAAGCCTTTCCTTCAAGTCACTCTTAGTCAT	528 709 588	Qy 529 TTCGACATGCTGAGCCTC	Qy         409 ACAAACGACCCTAAATGGT	Qy 289 GGTGAGCTTGTGGGTATC	Query Match  Best Local Similarity 77.3%;  Matches 486; Conservative  Qy 229 GGTGGCTGGCAGAGCGGCC
#_# #_# #_# 6_6 #_# 6_8 a	GTCTCCTTTCCTAGGGTACCATGTATGAAGAAAAGTGGAGTGAGT	TACCATGTATGAAGAAAGGTGGAGTGAGGTTTACAATC)	TTCGACATGGCTGAGCCTGCCTTCCTTCAAATCGCTCAATACCGAGCTGGTATCGTCCCC	ACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAACTTTTGC	GGTGGAGCTTGTGGGTATTGGGAATTTATACAGCCAAGGGTATGCACGACACCGTGGCGGAGCACCACCGTGGCGGAGCACCACCGTGGCGGAGCACCACCGTGGCGGAGCAGCACCACCAGCAGCAGCAGCAGCAGCAGCAG	40.5%; Score 401.8; DB 14; Length 736; imilarity 77.3%; Pred. No. 2.4e-53; conservative 0; Mismatches 143; Indels 0; Gaps GGTGGCTGGCAGAGCGCACCACCTTTTATGGTGGTGACGCATCTTGGCACCATG

Search completed: December 18, 2003, 22:32:00 Job time : 2068 secs

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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992 bp mRNA (Cs-EXP1) mRNA,

linear PL complete cds.

PLN 04-DEC-1996

ALIGNMENTS

Cucumis sativus expansin U30382 U30382.1 GI:1040874 Cucumis sativus (cucumber)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

1 (Dases 1 to 992)

Shcherban, T.Y., Shi, J., Durachko, D.M., Guiltinan, M.J., McQueen-Mason, S.J., Shieh, M. and Cosgrove, D.J.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular cloning and sequence analysis of expansins--a highly conserved, multigene family of proteins that mediate cell wall extension in plants Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995) 96016146
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Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                       Berendes, F., Rast, H.G., Vogt, U. and Gouloudis, C. Method for producing recombinant expansins Patent: WO 0188163-A 1 22-NOV-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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HSVSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVÞSNWQF
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Patent Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
                          Cucumis sativus (cucumber)
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Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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                                                                                                                          CAAAACTGGCAAAGCAACAACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCTT
                                                                                                                                             CAAAACTGGCAAAGCAACAACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCTT
                                                                                                                                                                                                         CACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGC
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ACCTATGAAGGCCCTCAATTC
                                      AGTGATGGTCGCACTCTCACTGCCTATAATCTCGTTCCTACCAATTGGCAATTTGGCCAA
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nilarity 99.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="Dyggwosghatfygggdasgtmggacgygnlysogygtntvals talfunglscgacfemtctndpkwclpgtirvtatnfcppnfalpnunggwcnpplqh fdmagsaflojagyragivpvsfrrvpcmkkggvrftinghsyenvlultnvcgaagdv hsvsikgsrtgwoskrnwgonwosnnylngoglsfqvtlsdgrtltaynlvpsnwqf ggtyegp0"

178 c 164 g 178 t
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/mol_type="genomic DNA"
/db_xref="taxon:3659"
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/db_xref="GI:17645713"
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Pred. No. 1.6e-174;
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Best Local S
Matches 582
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; rosids; eurosids I;
Rosales; Rosaceae; Amygdaloideae; Prunus.
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U93167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vegetaux, INRA, Site AGROPARC, 3 (bases 1 to 1109) Mbeguie-A-Mbeguie, D., Gomez, R.
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Mbeguie-A-Mbeguie,D.,
Molecular cloning and
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                                                                                      ATGGTGCTTTTGCT
                                                                                                                      TT--CACCTTCGCTGACTACGGTGGCTGGCAGAGCGGCCACCGTTTTATGGTGGTG
                                                                                                                                                      CTCAGGCATTGTCTTTAGCTCCCCTAGCCCTCTCTCTTGTTCTCTTCAATCTTCATCTTC
                     GTGATGCCTCGGGAACCATGGGGGAGCATGTGGGTATGGGAACTTGTACAGCCAAGGGT
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                                                                                                                                                                                                                                                                                                         /product="expansin"
/product="expansin"
/product="fac33529.1"
/protesin_id="AAC33529.1"
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**CFATMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEMECNNDPRWCRPGSII
**TATMFCCPNFAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIVPYTFRRVPCMKK
GGIRFTINGHSYENLVLITNVGGAGDVHSVSIKGSRTGWQPMSRNWGQNWQSNNYLNG
GSISEQVTISUGGTVTSYNVAPQNWQFGQTFSGGQF"
GSISEQVTISUGGTVTSYNVAPQNWQFGQTFSGGQF"
gSISEQVTISUGGTVTSYNVAPQNWQFGQTFSGGQF"
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/dev_stage="ripe fruit"
1. .1109
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/clone="pAPRI45"
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[mol_type="mRNA"
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Pred. No. 3.4e-113;
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Nicotiana
                                                                                               Link, B.M. and Cosgrove, D.J.
Direct Submission
Submitted (20-FEB-1998) Biology, Pennsylvania
Mueller Laboratory, University Park, PA 16802,
Location/Qualifiers
                                                                                                                                                                                                                                  Link, B.M. and Cosgrove, D.J. Acid-growth response and alpha-expansins bright yellow 2 tobacco Plant Physiol. 118 (3), 907-916 (1998)
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamidas; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1177)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGGTTTACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAAACGTCGGTG
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                                                                                                                                                                                    (bases 1 to 1177)
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note="suspension culture"
                 /cultivar="BY2"
/db_xref="taxon:4097"
                                                                 organism="Nicotiana
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                                                 _type="mRNA"
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CCTATAATCTCGTTCCTTCCAATTGGCAATTTGGCCAAACCTATGAAGGCCCTCAATTCT
                                   ATCTCAATGGCCAGAGTCTTTCATTTCAAGTCACCACTAGTGATGGAAGGACTCTCACTA
                                                           ATCTCAATGGCCAAGGCCTTTCCTTTCAAGTCACTCTTAGTGATGGTCGCACTCTCACTG
                                                                                                            CTAATACTGGATGGCAAACAATGTCCAGAAATTGGGGCCAAAACTGGCAGAACAATGCTA
                                                                                                                                                CTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGCCAAAACTGGCAAAGCAACA
                                                                                                                                                                                                                           TCGTTTTGATCACAAACGTCGGTGGCGCAGGCGACGTCCACTCTGTGTCGATAAAGGGGT
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/protein id="AAC96081.1"
/protein id="AAC96081.1"
/db xref="GI:4027899"
/translation="AFFSIISLLFFFFFSFCFHATFADYGGWQNAHATFYGGGDASGTM
/translation="AFFSIISLLFFFFFSFCFHATFADYGGWQNAHATFYGGGDASGTM
GGACGYGNLYSGGYGTWTAALSTALFNNGLTCGACYELTCNNDGQSCLQGSIIVTATN
FCPPNPSLPNNNGGWCNPFLQHFDLAQPAFLQIAKYRAGIVPVSFRVPCRRKGGVRF
TINGHSFFNLYLVTNVGGAGDVQSVSIKGSNTGWQTWSRNWGQNWQNNANLNGQSLSF
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/product="alpha-expansin"
221 c 256 g 372
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/function="involved in acid-growth response"
/note="cell wall protein"
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Pred. No. 6.3e-112;
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Pyrus communis PcExp2 mRNA fc
AB093029
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Direct Submission
Submitted (08-OCT-2002) Kyoko Hiwasa, Okayama University, Graduate
School of Natural Science and Technology; Tsushima-naka 1-1-1,
Okayama, Okayama 700-8530, Japan
(E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:81-86-251-8338,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrus communis (pear)
Pyrus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hiwasa,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
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                                                         GGTGGATGGGAGGGCGATGCCACATTTTATGGTGGTGGTGATGCCTCTGGCACAATG
                                                                       GGTGGCTGGCAGAGCGGCCACCTTTTATGGTGGTGATGGTACGCATCTGGCACCATG
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                                                                                                                   Conservative
                                                                                                                                                                                                                                              /gene="PcExp2"
/evidence=not_experimental
258 c 281 g 305
                                                                                                                                                                                                                                                                                                                     /product="expansin"
/protein_id="BAC67189.1"
/db_xref="GI:29467501"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="softening fruit"
/dev_stage="ripening fruit"
/country="Japan"
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/cultivar="La France"
/db_xref="taxon:23211"
                                                                                                                                                                                                                                                                                                                                                                                                          'gene="PcExp2"
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Pred. No. 4.7e-111;
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Pyrus con
AB093028
                                                                                    Submitted (08-OCT-2002) Kyoko Hiwasa, Okay School of Natural Science and Technology; Okayama, Okayama 700-8530, Japan [E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:6
                                                                                                                                                                                                               Pyrus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
                                                                                                                                                              Hiwasa,K., Rose,J.K., Nakano,R., Inaba,A. and Kubo,Y. Differential expression of seven alpha-expansin genes and ripening of pear fruit uppublished
                                                                                                                               2 (bases 1 to 1243)
Hiwasa, K., Kubo, Y., Nakano, R.
Direct Submission
                                                                              Fax:81-86-251-8338)
                                                                                                                                                                                                                                                               Pyrus communis (pear)
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/organism="Pyrus communis"
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School of Natural Science and Technology;
Okayama, Okayama 700-8530, Japan
(E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="softening fruit"
/dev_stage="ripening fruit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         country="Japan"
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Pred. No. 1.7e-110;
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            /gene="EXP2"
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/gene="EXP2"
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TAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCAACTTTTGCCCTCCTAACTT
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Direct Submission Submitted (19-FEB-2001) Department of Horticulture, Michigan St University, 392A Plant and Soil Science Building, East Lansing, Prunus cerasus expansin AF350937 Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 1109) Yoo,S.-D. and van Nocker,S. Prunus cerasus Prunus cerasus (bases 1 to 1109) /organism="Prunus cerasus"
/mol type="mRNA"
/mol type="taxon:140311"
/tlssue type="ripening fruit"
/note="sour cherry" ocation/Qualifiers Gao, Z., Cantini, C., Loescher, W. and van GI:13898650 1109 b (EXP2) ğ mRNA, mRNA RNA linear complete cds Nocker, S. PLN 01-MAY-2001 ng, MI

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ATCAGCCACACTGCTA 927
                             CGTGGCCCCTGGTAATTGGCAGTTTGGTCAGACTTTCTCAGGGGGTCAATTTTAGAGTTA
                                                           TCTCGTTCCTTCCAATTGGCCAATTTGGCCAAACCTATGAAGGCCCTCAATTCTAAACCAT
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/protein_id="AAK48846.1"
/db_xref="GI:13898651"
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Wu, Z. and Wiersma, P.A.
Direct Submission
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TAGATGGTGTCGTCGGAAGCATCATTGTTACTGCTACAAACTTTTGCCCACCTAACTT
                              TAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCCACCAACTTTTGCCCCTCCTAACTT
                                                                                    GCTATTTAACAATGGATTAAGTTGTGGGTGCTTGGTTCGAAATGACTTGTACAAACGACCC
                                                                                                                                                   TGGGTATGGGAATTTATACAGCCAAGGGTATGGCACGAACACGGTGGCGCTGAGCACTGC
                                                                                                                                                                                              AGGCGCTCATGCCACTTTTTATGGTGGCGGTGATGCCTCGGGAACAATGGGGGGAGCATG
                                                                                                                                                                                                                 GAGCGGCCACGCCACCTTTTATGGTGGTGGTGGTGACGCATCTGGCACCATGGGTGGAGCTTG
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                                                                                                                                                                                                                                                                                  TTCCACTAGATTATTA
                                                                                                                             TGGGTATGGGAACTTGTACAGCCAGGGTATGGAACCAACACTGCAGCTTTAAGCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                               Conservative
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/rodor_start=1
/codon_start=1
/product="expansin 1"
/protein_id="AAG13982.1"
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GSISEQVTISDGRTYTNVAVAEGNWQFGQTFSGGQF"
GSISEQVTISDGRTYNVAVAEGNWQFGQTFSGGQF"
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81. .845
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                                                                                                                                                                                                                                                                                                                                             439.2; DB 8;
No. 2.1e-109;
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Reina
                                                                                                                                                                                                                     Direct Submission
Submitted (15-DEC-2000) Labrador E., Dpto.
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae;
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expansin
Cicer arietinum (chickpea)
Cicer arietinum
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Cicer arietinum mRNA for
AJ291817
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An second (
                                                                                                                                                                                                                                                                                                                                     Cicer
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                                                                                                                                                                                                                                                              Labrador,
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                                                                                                                                                                                                                                                                                                 , Sanchez,
           /codon_start=1
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/db_xref="GI:11932092"
                                                                                               /db_xref="taxon:3827"
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/tissue_type="etiolated
/clone_lib="CAN-5"
                                                                                                                                                 /organism="Cicer arietinum"
/mol_type="mRNA"
/cultivar="Castellana"
                                                                                                                                                                                                Location/Qualifiers
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                                                                country="Spain"
                                                                                                                                                                                                                                                                                                            M.A.
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expressed in chickpea
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AY083166.1
              Malus x domestica (apple tree)
Malus x domestica
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots;
            Spermatophyta; Magnoliophyta; rosids; eurosids I; Rosales; F
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                                    GCCAAACCTATGAAGGCCCTCAATTCTAAA
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GTCAAACATTTCAAGGAGCTCAATTTTAGA
                                                                               CCACAAGTGATGGTAGAACTATGACAAGTTACAATGTGGCCCCATCCAATTGGCAATTTG
                                                                                                     CTCTTAGTGATGGTCGCACTCTACTGCCTATAATCTCGTTCCTATCCAATTGGCAATTTG
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KPGSIIVTATNECPPNESLANNNGGWCNPPLGHEDMAEDAFLOLAEYRAGIVPVSFRR
VPCMKKGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSIKGSRTGWQSMSRNWGQNWQS
NSYLNGQDLSFQVTTSDGRTMTSYNVAPSNWQFGQTFQGAQF"
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2.7e-109;
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domestica expansin

1108 in 1

bp mRNA linear PLN (EXP1) mRNA, complete cds.

linear

NTd

10-APR-2002

GI:20135549

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 757
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Trivedi, P.K. and Solomos, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trivedi, P.K. and Solomos, T. Characterization of expansin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Landscape Architecture,
                                                                                         ACAATCAATGGCCACTCATACTTCAACCTCGTTTTGATCACAAACGTCGGTGGCGCAGGC
                                                                                                                                                                                          CCTCTCCAACACTCCGACATGGCTGAGCCTGCCTTCCAAATCGCTCAAATACCGAGCT
                                                                                                                                                                                                                                                 ACCAACTTTTGCCCTCCTAACTTTGCTCTCCCTAACAACAATGGTGGATGGTGCAACCCT
                                                                                                                                                                                                                                                                                                    GAAATGACTTGTACAAACGACCCTAAATGGTGCCTTCCGGGAACTATTAGGGTCACTGCC 456
                                                                                                                                                                                                                                                                                                                                                     TGGGGCCAAAACTGGCAAAGCAACAACTATCTCAATGGCCAAGGCCTTTCCTTTCAAGTC
                                                GACGTCCACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAAT 756
                                                                                                                                                   GGTATCGTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTT
                                                                                                                                                                                                                                ACAAACTTTTGCCCTCCTAACTTTGCTGAGTCCAACGACAATGGCGGATGGTGCAATCCT
                                                                                                                                                                                                                                                                                   GAAATGATGTGCAACAATGACCCGAGATGGTGCCGTCCTGGATCCATTATTGTTACTGCT
                                                                                                                                                                                                                                                                                                                                    AACACTGCAGCTTTGAGCACAGCATTGTTCAACAATGGCTTGAGCTGTGGATCTTGTTAT 299
                                                                                                                                                                                                                                                                                                                                                                                        TCGGCAACAATGGGAGGAGCATGTGGTTATGGGAATCTGTACAGCCAGGGATATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                TCTGGCACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGCCAAGGGTATGGCACG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCTGTTTATGGTAGCTGGGAAGGCGTTCATGCCACATTTTACGGCGGCGGTGATGCC 179
                                                                                                                            GGAATCGTGCCGGTTTCCTTCAGAAGAGTACCTTGTATGAAGAAAGGAGGAATAAGATTC
                                                                                                                                                                             CCTCTCCAGCACTTCGATTTGGCCGAGCCTGCTTTCTTGCAGATTGCTCAATACCGCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Malus x domestica"
/mol type="mRNA"
/cultivar="Granny Smith"
/db_xref="taxon:3750"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="EXP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="ripening fruit pulp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%;
76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 435; DB 8;
Pred. No. 3e-108;
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University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1108;
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Matches 536
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322 CAAGGGTATGGCACGAACACGGTGGCGCTGAGCACTGCGCTATTTAACAATGGATTAAGT
                                                                                                                                   202
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                                                                                                                                                                    536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-2002) Department of Environmental Horticulture, University of California, Davis, One Shields Avenue, Davis, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY079206
Mirabilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gookin, T.E., Hunter, D.A. and Reid, M.S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gookin, T.E., Hunter, D.A. and Reid, M.S.
Temporal analysis of alpha and beta-expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Nyctaginaceae; Mirabilis.
1 (bases 1 to 1262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mirabilis jalapa (garden four-o'clock)
Mirabilis jalapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     floral opening and senescence
Plant Sci. 164 (5), 769-781 (2003)
2 (bases 1 to 1262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY079206.1
                                                                                                                                                                                  Similarity
                               GGTGGAGGAGATGCTTCTGGCACCATGGGGGGGGCTTGTGGATATGGGAACTTGTACAGT
                                                     GGTGGTGGTGACGCATCTGGCACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACAGC
                                                                                                 TTTGCTGGTGTCAATGCCGGCTATGATGGCGGTTGGACAACTGCTCATGCCACTTTTTAT
                                                                                                                           TTCTTTGTCTTCACCTTCGCTGACTACGGTGGCTGGCAGAGCGGCCACGCCACCTTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCAGACATTCTCAGGGGGGGCAATTTTAGAATTATTCCACTAGACT
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                                                                                                                                                                                                                                          760.
201
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LSFQVTASDGRTVTSNNIAPANWQFGQTYVGAQF"
                                                                                                                                                                                                                                                                                                                           /db xref="GI:28524706"
/translation="MTYYPTLFTTLVIVIHVWFAGVNAGYDGGWTTAHATFYGGGDAS
/translation="MTYYPTLFTTLVIVIHVWFAGVNAGYDGGWTTAHATFYGGGDAS
GTMGGACGYCNLYCQGYGTWTAALSTALFTNALFCCSCYSCYSMKCNDDFKWCRPGSIVVT
ATNFCPPNYALANNNGGWCNPPLQHFDMACPAFLQAGYRAGIVPISFRRYPCAKKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="expression similar to during senescence"
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="cell wall prote
/protein_id="AAL87023.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="petal-like calyx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mirabilis jalapa"
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                                                                                                                                                                                 43.4%;
75.4%;
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201 c
                                                                                                                                                                   <u>.</u>
                                                                                                                                                                 Score 431; DB 8;
Pred. No. 3.8e-107;
0; Mismatches 175;
                                                                                                                                                                                                                                                   281
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                                                                                                                                                                                                                                                   416
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                                                                                                                                                                                              Length 1262;
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Search completed: December 18, 2003, 21:57:22 Job time : 3655 secs

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Result
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                            pred. No. is the score greater to and is derived
                                                                                                                                                                                                                                     Score
         1275
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1041
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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1394
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                            AAR94527
AAG80768
AAG80769
ABB98474
AAG25443
AAG46483
AAG46483
AAG06546
                                                                                                                                                                                                                                                                                                    SUMMARIES
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Cucumber expansin-
C. sativus S1 expa
C. sativus expansi
Plant expansin con
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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DR XXX PR PR XXX PR XXX

WPI; 1996-201150/21. N-PSDB; AAT13320.

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Best Local S
Matches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. It can be obtd. by expression of an isolated cDNA clone (see AAT1330) in bacterial or other host cells. Expansin proteins have also been identified in oat coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29), and appear to be broadly distributed throughout the plant kingdom. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel mechanical strength, etc.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                   19-APR-2002
                                                                                                                                                                                                                                                                                                                                           AAG80768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expansin proteins which alter the mechanical strength poly:saccharide(s) - useful in paper mfr. and recycli
 Vector encoding an expansin, useful in treatment of cellulosic
                                                                Berendes F,
                                                                                                                   16-MAY-2000; 2000DE-1023561.
                                                                                                                                                                                                DE10032630-A1
                                                                                                                                                                                                                          Cucumis sativus
                                                                                                                                                                                                                                                  paper pulp;
                                                                                                                                                                                                                                                              Expansin;
                                                                                                                                                                                                                                                                                                                                                                     AAG80768 standard;
                                                                                                                                             05-JUL-2000; 2000DE-1032630
                                                                                                                                                                       22-NOV-2001
                                                                                          (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                        sativus S1
                          2002-155755/21
DB; ABA97161.
                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYGGWQSGHAT FYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expansin-29 (AAR94527) is a member of a novel class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                   QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
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                                                                                                                                                                                                                                                              $1;
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                                                                Rast HG,
                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                 cellulose-based textile; cotton; paper recycling; lant tissue; papermaking; cucumber.
                                                                                                                                                                                                                                                                                       expansin homologue fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.5%; L.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                     Protein; 227
                                                                                                                                                                                                                                                                                                                  entry)
                                                                Vogt U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1275; DB 17;
Pred. No. 3.1e-118;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     8
                                                                   Gouloudis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trength of recycling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of extensins possible. This sequence represents the Cucumis sativus (cucumber) S1 extensin homologue fragment
                                                                                                                                                                                                                                                                                                                                                                                 C. sativus expansin csexpla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG80769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     described
          Example 1; Page 14-16; 22pp; German
                                      Vector encoding an expansin, useful in treatment of cellulosic materials for paper recycling, providing large-scale production
                                                                                                                                 Berendes
                                                                                                                                                                                       16-MAY-2000; 2000DE-1023561
                                                                                                                                                                                                                    05-JUL-2000; 2000DE-1032630
                                                                                                                                                                                                                                                                              DE10032630-A1
                                                                                                                                                                                                                                                                                                           Cucumis sativus
                                                                                                                                                                                                                                                                                                                                     paper pulp; plant
                                                                                                                                                                                                                                                                                                                                                      Expansin; cellulose-based
                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG80769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             materials for paper recycling, providing large-scale production
                                                                                                                                                                                                                                                 22-NOV-2001.
                                                                                                                                                           (FARB ) BAYER
                                                                                                    2002-155755/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                     ABA97162
                                                                                                                               F, Rast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTNDEKWCLEGTIRVTATNECEPENEALENNNGGWCNEPLQHEDMAEEAFLQIAQYRAGI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 11-14; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                               <del>ظ</del>
                                                                                                                                                                                                                                                                                                                                     se-based textile; cotton; paper recycling; csexpla;
tissue; papermaking; cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.5%; Score 1275; DB 23; 100.0%; Pred. No. 3.1e-118;
                                                                                                                              Vogt
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Example 1; Fig

2 20pp;

English.

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RESULT 4
ABB98474
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Best Local
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                    Novel swollenin protein isolated from applications in cleaning textiles (lau compositions), modifying textiles (departing textiles)
                                                                                                                                                                                                                                                                                                                                                          Longibrachiatum; filamentous fungus; swollenin; cotton fibre swelling; cellulose; cellulosic substrate; animal food; biomass; glucose; paper manufacture; laundry detergent; plant; expansin.
           anti-greying)
                                                                               WPI; 2002-642241/69.
                                                                                                                                                                (WARD/)
(PENT/)
                                                                                                                                                                                                                      11-JUL-1997;
                                                                                                                                                                                                                                                 09-JUL-1998;
                                                                                                                                                                                                                                                                             04-JUL-2002
                                                                                                                                                                                                                                                                                                        US2002086350-A1
                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                    Plant expansin consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB98474 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                             (SWAN/)
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                                                                                                                                   WARD M.
PENTTILA M.
JAAKKO P.
SALOHEIMO M.
                                                                                                        BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                         SWANSON B A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI
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                                                                                                         Ward M,
                                                                                                                                                                                                                      97US-0893766
                                                                                                                                                                                                                                                 98US-0112498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.0%; Score 1269; DB 23; 100.0%; Pred. No. 1.2e-117;
                                                                                                           Penttila
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                       (depilling,
                                    rom fungus or bacteria, has (laundry detergents and pre-wash
                                                                                                         Jaakko
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                        color
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                        restoration,
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RESULT 5
AAG25443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc cellulclytic activity i.e., catalytic activity involving the breakage of condividual cellulose strands into smaller monomer (glucose) or oligomers (polysaccharides). Swollenin and its coding sequence are useful in certably contents of altering the properties of cellulosic substrate. Preferably ct methods for altering the properties of cellulosic substrate. Preferably ct methods are useful for altering the nutritional properties of animal cellulosic substrates of animal substrates, altering properties of cellulosic biomass during the reduction to glucose. The swollenin coding sequence has utility in cellulosic corn husk fibre during its reduction to glucose. The swollenin coding sequence has utility in cellulase is currently used, for example, company applications for which cellulase is currently used, for example, company applications for which cellulase is currently used, for example, compositions, and compositions, and consensus sequence is expressed by a fungus, it can be produced in large cuantities. The present sequence is a consensus sequence for plant composition, which was used in a sequence alignment with a partial swollenin composition sequence. It was found that there was a 21.7% identity between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                   06-SEP-2000
                                                                                                                                                       EP1033405-A2
                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to swollenin from Trichoderma reesei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWQSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFELTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 85
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99US-0121825.
99US-0123180.
99US-0123548.
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88.4%; Pred. No. 5.9e-104;
tive 16; Mismatches 8;
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RESULT 6
AAG46483
ID AAG4
XX AAG4
AC AAG4
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XX AAG4
XX AG4
XX Prot
XW Prot
XW Prot
XW Lerm
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28-OCT-1999
                                                         Protein identification; signal transduction hybridisation assay; genetic mapping; gene of
                                                                                                  Arabidopsis
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                   Arabidopsis
                                              termination
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||:|||||: |: :: ||||||
VHAVSIKGSKTQSWQAMSRNWGQNWQSNSYMNDQSLSFQVTTSDGRTLVSNDVAPSNWQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                          LQHFDMABPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGD
                                                                                                  thaliana
                   thaliana
                                              sequence
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9908-0158329

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9908-015933

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9908-016963

9908-0160741

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9908-0160768

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9908-0160981

9908-0161981

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77.9%;
                                                                                                   protein fragment
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Pred. No. 2.6e-99;
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                                                                                                   SEQ
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                                                         n pathway; metabolic expression control;
                                                                                                   NO:
                                                                                                     58485
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                                                         pathway;
promoter;
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05-MAR-1999
09-MAR-1999
23-MAR-1999
23-MAR-1999
01-APR-1999
01-APR-1999
11-APR-1999
23-APR-1999
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99US-0121825.
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99US-0125788.
99US-0126785.
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99US-0126785.
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99US-013049.
99US-013049.
99US-0132486.
99US-013255.
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01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 08-JUL-1999;

09-JUL-1999;
13-JUL-1999;
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RESULT 7
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22-SEP 1999
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113-OCT 1999
113-OCT 1999
114-OCT 1999
114-OCT 1999
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121-OCT 1999
17-OCT-2000
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                                                                                                                                                                                                                                                                                                                                        standard;
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S-0161406.
S-0161359.
S-0161361.
S-0161361.
S-0161920.
S-0161920.
S-0161993.
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                                                               Protein;
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Arabidopsis the protein identify hybridisation termination see arabidopsis the EP1033405-A2.  06-SEP-2000.  25-FEB-1999; 05-MAR-1999; 05-MAR-1999; 06-APR-1999; 06-APR-1999; 19-APR-1999; 19-APR-1999; 11-APR-1999; 11-JUN-1999; 1
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pathway; metabolic pathway; expression control; promoter;
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pathway; promoter;

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Local Similarity 79.6%;
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23; Mismatches 23;
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SEQ ID

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79.6%;
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Pred. No. 5.6e-95;
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Best Local Similarity 79.6%;
Matches 179; Conservative
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65550 way; metabolic pathway; ssion control; promoter;	FDMAEPAFLQIAQYRAGIVP 145    : :              : :
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74.7%; Score 1041; DB 21; 79.6%; Pred. No. 5.9e-95; tive 23; Mismatches 23;
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9908-0127462

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79.6%;
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Pred. No. 5.9e-95;
3; Mismatches 23
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expression control; promoter;
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99US-014933.
99US-014933.
99US-014933.
99US-014933.
99US-014933.
99US-014935.
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RESULT 14
AAG51631
XX AAG51
XX AAG51
XX AAG51
XX AAG51
XX AAG51
XX AFAbi
XX Prote
XW Hybri
XX AFAbi
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Best Local Sim
Matches 179;
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

26-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

06-MAY-1999

06-MAY-1999

07-MAY-1999

07-MAY-1999

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07-MAY-1999
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Similarity 79.6%;
79; Conservative :
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99US-0126785

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promoter;
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28-UIL-1999
02-AUG-1999
02-AUG-1999
03-AUG-1999
04-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
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99US-0146386 99US-0146389 99US-0146389 99US-0147702 99US-0147703 99US-0147703 99US-0147703 99US-0147703 99US-0147703 99US-0147703 99US-0147703 99US-0148119 99US-0148119 99US-0148119 99US-0148119 99US-0149722 99US-0149722 99US-0149722 99US-0149723 99US-0149723 99US-0149723 99US-0150866 99US-0160814 99US-01610086 99US-01610088 99US-01610088 99US-01610088 99US-01610088 99US-01610088

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19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999;	11-MAY 1999 11-MAY 1999 21-MAY 1999 01-JUN 1999 01-JUN 1999 11-JUN 1999	-MAY-199
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RESULT 15
AAG51645
ID AAG51
XX AAG51
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XX Prote
XW Prote
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Best Local Sim
Matches 179;
   25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

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25-OCT-1999;
25-OCT-1999;
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26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                         25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEBAFLQIAQYRAGIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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nilarity 79.6%;
Conservative 2
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   99US-0121825

99US-0123548

99US-0125788

99US-0126784

99US-0126786

99US-0126786

99US-0127462

99US-0128234

99US-0128234

99US-0128077

99US-0130077

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99US-0161405
99US-0161405
99US-0161406
99US-0161359
99US-0161361
99US-0161361
99US-0161920
99US-0161992
99US-0161993
99US-0161993
99US-0161993
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06-MAY-1999
06-MAY-1999
06-MAY-1999
11-MAY-1999
11-JUN-1999
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99US-0132485
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99US-0132863
99US-0134271
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01-SEP 1999
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99US-0145087

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                                                                                                                Similarity 79.6
79; Conservative
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WQSNNYLNGQGLSFQVTLSDGRTILTAYNLVPSNWQFGQTYEGPQF
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99US-0160980.
99US-0160999.
99US-0161404.
99US-0161406.
99US-0161359.
99US-0161359.
99US-0161350.
99US-0161920.
99US-0161920.
99US-0161920.
99US-0161920.
                                                                                                                      74.7%;
79.6%;
                                                                                                               Score 1041; DB 21;
Pred. No. 6.9e-95;
3; Mismatches 23;
                                                                                                                             Length 280;
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Gaps

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145 114 85

234 205 174

Search completed: December 18, Job time: 43 secs 2003, 17:48:29

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein -
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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Best Local :
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FILING DATE: 11-UUL-1997
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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227; Conserv
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sequence 5, Appli	ຸທ	Sequence 24, Appl	Sequence 24, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli	•	Sequence 15, Appl	-	Sequence 21, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 2, Appli				

## ALIGNMENTS

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TITLE OF INVENTION: MICROBIAL SWOLLEN
TITLE OF INVENTION: ENCODING SUCH SW
TITLE OF INVENTION: SWOLLENINS
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VG
CURRENT APPLICATION NUMBER: US/09/112,498A
181
                                                                                                                                                                             84 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI
                                                                                                                                                                                                                                                    24 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM
QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
                        QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVDSNWQPGQTYBGPQF 250
                                                                         VPVSFRR VPCMKKGGVR FTINGHSY FNLVLITNVGGAGDVHSVSI KGSRTGWQSMSRNWG
                                                                                               VPVSFRR VPCMKKGGVR FT I NGHS Y FNLVLI TNVGGAGDVHS VSI KGSRTGWQSMSRNWG
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100.0%; Prr
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                                                                                                                                                                                                                                                                                                                                                  Length 227;
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METHOD OF PRODUCING SUCH
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OTHER INFORMATION: expansin
US-09-092-160-7
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 7
LENGTH: 227
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                                                    TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA
TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND MET
TITLE OF INVENTION: SWOLLENINS
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EF
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09112498A Patent No. 6458928
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER APPLICATION NUMBER: 08/060,944
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT:
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
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                                       APPLICATION NUMBER:
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APPLICATION DATA:
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                                       US/09/112,498A
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Pred. No. 8.3e-116;
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US-09-112-498A-11
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FILING DATE: 11-UUL-1997
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0
FILING DATE: 11-JUL-1997
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MICH
TITLE OF INVENTION: SWOI
TITLE OF INVENTION: SWOI
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: UPPLICATION APPLICATION DATA:
APPLICATION NUMBER: UPPLICATION NUMBER: UPPLICATION NUMBER: UPPLING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                        LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                         TOPOLOGY:
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No. 6458928
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                                                                                                  h 74.2%;
Similarity 78.1%;
78; Conservative 23
                                                                                                                                                                                                                      : 233 amino acids amino acid
                                                  ADYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
MTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
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                                 ADYGSWQSAHATFYGGGDASGTMGGACGYGNLYSTGYGTNTAALSTVLFNDGAACRSCYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WQSNSYLNGQSLSFQVTLSDGRTVTS-NVAPANWQFGQTF-GGQF 223
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                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                            US 08/893,766
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; Pred. No. 9.9e-103;
16; Mismatches 8;
                                                                                                     23;
                                                                                                  Score 1035; DB 4;
Pred. No. 2.5e-93;
3; Mismatches 27
                                                                                                                                      DB 4;
                                                                                                     27;
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                                                                                                                                    Length 233;
                                                                                                     Indels
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US-08-440-517A-2
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US-09-112-498A-7
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                                                  Sequence 2, Application US/08440517A
Patent No. 5959082
GENERAL INFORMATION:
APPLICANT: COSCROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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APPLICATION NUMBER: US 98/14226
FILING DATE:
APPLICATION NUMBER: US 08/893,766
FILING DATE: 11-TUL-1997
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112.4987
PILING DATE:
PRIOR APPLICATION NUMBER: US/09/112.4987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MICH
TITLE OF INVENTION: ENCO
TITLE OF INVENTION: SWOJ
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
                     APPLICANT:
 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 177; Conserv
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amino acid
                                                                                                                                                                                                                                              WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ 249
                                                                                                                                                                                                                                                                                                                    VSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN 205
                                                                                                                                                                                                                                                                                                                                                                      QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 131
                                                                                                                                                                                                                                                                                                                                                                                             TNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNW 202
                                                                                                                                                                                                                   WQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQ
                                                                                                                                                                                                                                                                                               VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFXQTFEGGQF
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                 SHI, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%;
PURIFIED EXPANSIN PROTEINS
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Pred. No. 5e-93;
3; Mismatches 24;
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                                                                                                               APPLICANT: Shi, Jun

APPLICANT: Shi, Jun

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION UNMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION UNMBER: 08/440,517
EARLIER APPLICATION UNMBER: 08/242,090
EARLIER FILING DATE: 1995-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1993-05-12
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                                                                     SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 2, Application US/09092160C Patent No. 6255466
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
                                                                                                           NUMBER OF SEQ ID NOS:
LENGTH: 228
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
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LENGTH: 228
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TYPE: AMINO ACID
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ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                          PatentIn
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; Pred. No. 1.8e-92;
22; Mismatches 24;
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Best Local :
                                                                                                                                                                   Matches 178;
                                                                                                                                                                                 Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   FILING DATE: 11-JUL-1997
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa is unknown or other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                          TOPOLOGY: ur
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Dalan
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FILING DATE:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                    144
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VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
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                                                                          TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI
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78.1%;
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                                                                                                                                                                   26; Mismatches
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Pred. No. 1.8e-92;
                                                                                                                                                                                 Score 1022.5; DB 4;
Pred. No. 4.1e-92;
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METHOD OF PRODUCING SUCH
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             Sequence 6, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
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US-09-092-160-6
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RESULT 9
US-08-440-517A-6
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                                                                                                                                                                                                                                                                                    Matches 175;
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                         144
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                                 204
                                                                     120 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWG
 180
                                                                                                                                           60 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
                                                                                                                                                              84 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI 143
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                  QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                          VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
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QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF
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                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN
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                                                                                                                                                                                                                                                                                                         72.6%;
77.1%;
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                                                                                                                                                                                                                                                                                                         Score 1011.5; DB Pred. No. 4.7e-91;
                                                                                                                                                                                                                                                                                          Mismatches
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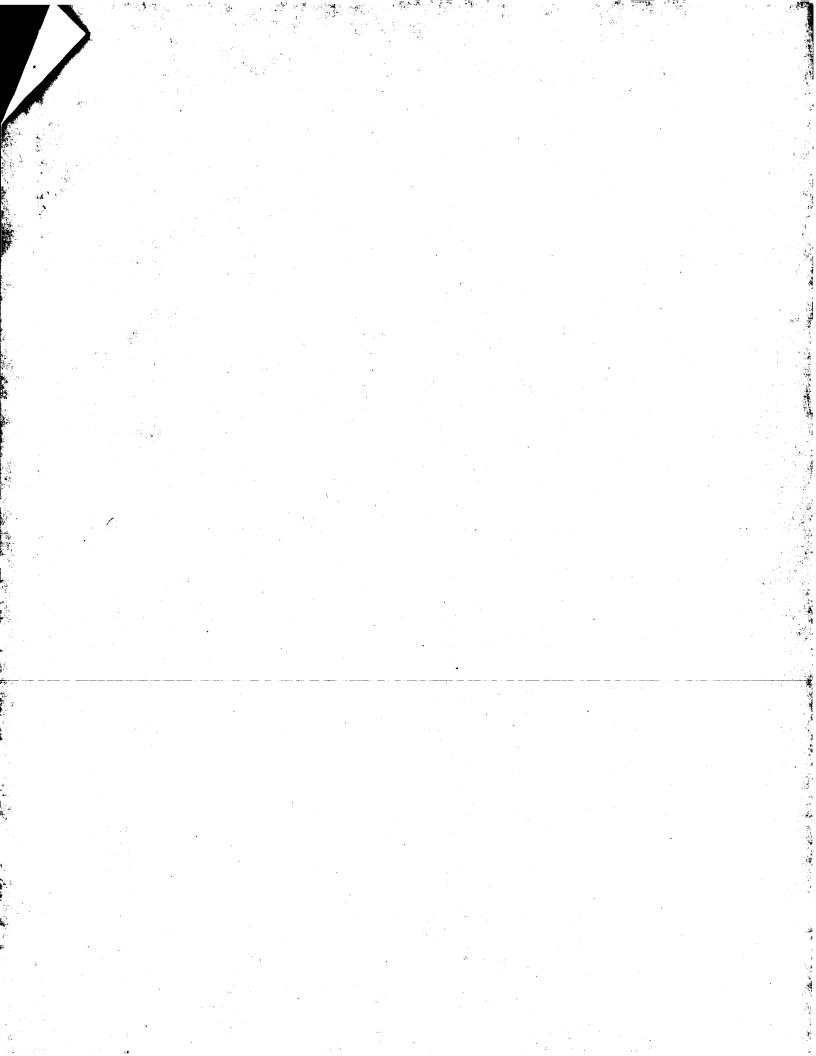
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Patent No. 5959082
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SEQ ID NO 6
LENGTH: 226
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Best Local S
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APPLICANT: COSGROVE, E
APPLICANT: GUILTINAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REF
CURRENT
CURRENT
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EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1993-05-12 NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHI, JUN TITLE OF INVENTION:
                                                                                                     COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                         STREET: 113 TECHNOLOGY CENTER CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 08/060,944
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                                                                                                                                                                                                      16802-7000
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CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF
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                                                                                                                                                                                                                                           PENNSYLVANIA
                                                                                                                                                                                                                      UNITED STATES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                              COSGROVE, DANIEL J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           SHCHERBAN, TATYANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1194/1C114US3
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77.1%; Pred. No. 4.7e-91;
cive 23; Mismatches 28
                                                                      US/08/440,517A
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                                                                                                                                                                                                                      AMERICA
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US-08-440-517A-5
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TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER FILING DATE: 1995-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
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Best Local S
Matches 171
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SEQ ID NO 5
SENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Patent No. 6255466
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Best Local Similarity
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7
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                                                                                                                              144 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTG-WQSMSRNW 202
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203 GQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
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171; Conservative
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                                                                         VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW
                                                                                                                                                                                                                                     TCEDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
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75.0%;
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Pred. No. 3
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Pred. No. 3.2e-86;
% Mismatches 27;
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US-09-112-498A-10
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US-09-112-498A-13
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Best Local S
Matches 161
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                                                                                                                                                                                                          Sequence 13, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-JUL-1997
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                            TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF SEQUENCES:
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TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
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6458928
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                                                                                                                                                                                                                                                                                                            QNWQSNSVLVGQSLSFRVTSSDRRSSTSWNIAPANWKFGQTFMGKNF
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                                                                                                                           MICROBIAL SWOLLENIN PROTEIN, ENCODING SUCH SWOLLENINS AND SWOLLENINS
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US/09/112,498A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 939; DB 4;
Pred. No. 6.2e-84;
9; Mismatches 35
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SWOLLENINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                            DNA SEQUENCES
METHOD OF PRODUCING SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPO)
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                                (EPO)
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HOD OF PRO
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US-09-112-498A-9
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                                                                                                                            US-09-112-498A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09112498A Patent No. 6458928
                                                                           Query Match
Best Local S
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Best Local Similarity
                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US
FILING DATE: 11-JUL-15
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-JUL-1997 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MICH
TITLE OF INVENTION: ENCO
TITLE OF INVENTION: SWOJ
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
                                                                                                                                         TYPE: amino i
TOPOLOGY: uni
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98/14226
FILING DATE:
APPLICATION NUMBER: US 08/893,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acid
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVCGAGDVHSVSIKGSRTGWQSMSRNWG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165;
                                                              157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 DODPRWCNPGNPSILITATNFCPPNFAEPSDNGGWCNPPRPHFDLAMPMFLKIAQYRAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GPWTSAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKC
14 GPWINAHATFYGGGDASGTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACFELMC
                         26 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNWQSNAVFVGQALSFRVTGSDRRTSTSWNVAPPHWQFGQTFTGKNF
                                                                                                                                                                                          233 amino acids
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                                                              Conservative
                                                                                                                                                           unknown
                                                                                                                                                                            acid
                                                                                                                                           protein
                                                                                                                                                                                                                                          MBER: US 08/893,766
11-JUL-1997
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72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MICROBIAL SWOLLENIN PROTEIN, ENCODING SUCH SWOLLENINS AND SWOLLENINS
                                                              63.8%; Score 889.5;
69.5%; Pred. No. 4e-
tive 26; Mismatches
                                                                                                                                                                                                                                                                                           US 98/14226
                                                                                                                                                                                                                                                                                                                                          US/09/112,498A
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Pred. No. 1.1e-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Version
                                                                                4e-79;
                                                                                          DB 4;
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                                                               Indels
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                                                                                               233;
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                                                               Gaps
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   73
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Search	ф	γQ	뮹	δ	Ф	Ş	
Search completed: December 18, 2003, 17:50:54	186 NWQSNSYLNGQSLSEVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 231	205 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250	126 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 185	145 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 204	74 VNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGII 125	86 TNDPKWCLPG-TIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 144	



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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-383-579C-10
1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
/cgn2_6/ptodata/2/pubpaa/US09Ā_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10Ā_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pubpaa/US07
/cgn2_6/ptodata/2/pubpaa/PCT_N
/cgn2_6/ptodata/2/pubpaa/US06
                                                                                                                                                                                                                                                                                                                        6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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1459.052 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                             NEW PUB.pep:*
NEW PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8 9 10 11 12 13 14 15	7 O U 4 U D 7	Result No.
1026 1017.5 1013.5 1011.5 962 940 937 889.5	1265 1228 1131 1109.5 1109.5 1044 1035 1027	Score
73.6 73.0 72.7 72.6 69.0 67.4 63.8	90.7 88.1 81.1 79.6 74.9 74.2	Query Match Length
228 236 226 225 237 237 233	2225 2225 2223 233	bength
15 15 15 15	125 125 125 125 125	DB
US-09-896-301-2 US-10-197-294A-8 US-10-197-294A-9 US-09-896-301-6 US-09-896-301-5 US-09-896-301-5 US-10-197-294A-11 US-10-197-294A-10	US-10-197-294A-6 US-10-197-294A-4 US-10-197-294A-4 US-10-197-294A-5 US-10-150-559-4 US-10-197-294A-12 US-10-409-701-9	ID
sequence 2, Appli Sequence 8, Appli Sequence 9, Appli Sequence 6, Appli Sequence 5, Appli Sequence 11, Appl Sequence 14, Appl Sequence 10, Appl	Sequence 7, Appli Sequence 6, Appli Sequence 4, Appli Sequence 5, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli	Description

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
	100.5	109.5	150.5	U	185	185.5	192.5	206.5	206.5	220.5	229	232	232.5	236.5	239	239	246	253.5	262.5	266.5	266.5	266.5	273	294	302.5	362.5	773.5	814	857.5	884
	7.2	7.9	10.8	10.8	13.3	13.3	13.8	4	14.8	15.8	16.4			17.0	17.1	7	17.6	œ	8	9	9	19.1	٩	۲	ŗ	26.0	'n	ω.	:	63.4
	5 <u>4</u>	138	493	322	191	190	263	222	222	269	263	231	265	240	263	263	283	239	265	282	282	282	245	308	299	247	227	232	222	234
	12	15	15	15	1	15	H	12	12	11	1	15	1	9	1	9	12	12	15	15	12	12	5	15	5	15	10	15	10	15
•	US-10-161-660-12	US-10-125-001-19	US-10-197-294A-2	US-10-197-294A-3	US-09-847-208-173	US-10-125-001-13	US-09-847-208-127	US-10-259-165-392	US-10-259-165-44	US-09-847-208-133	US-09-847-208-112	US-10-125-001-11	US-09-847-208-107	US-09-949-888-2	US-09-847-208-138	US-09-811-672-10	US-10-409-701-11	US-10-259-165-276	US-10-125-001-12	US-10-125-001-2	0-102-349-	US-10-102-349-2	US-10-125-001-14	US-10-125-001-4	US-10-125-001-22	US-10-125-001-20	US-09-896-301-4	US-10-197-294A-13	US-09-896-301-3	US-10-197-294A-7
	12,	e 19,	e 2,	w ۲	17		12	e 39:	44	13	11:	11	O	Sequence 2, Appli	æ	10,	Sequence 11, Appl	276	12	2	4	<u>ب</u>	e 14,	Sequence 4, Appli	e 22,	e 20,	4	Sequence 13, Appl	Ü	Sequence 7, Appli

## ALIGNMENTS

US-09-896-301-7

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; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cucumber; OTHER INFORMATION: expansin
US-09-896-301-7
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
Matches 225; Conservative
                                                                                                                                                                                                                                                               SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020103355A1
                        Query Match 90.7%;
Best Local Similarity 99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COSGTOVE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/092,160 PRIOR FILING DATE: 1998-06-05
                                                                                                                                                                                  LENGTH: 227
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09896301
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Score 1265; DB 10;
Pred. No. 2.4e-118;
2; Mismatches 0;
  Indels
                                            Length 227;
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Gaps

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RESULT 3
US-10-197-294A-4
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US-10-197-294A-6
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Sequence 4, Application US/10197294A
Publication No. US20030104546A1
GENERAL INFORMATION:
APPLICANT: Swanson, Barbara A.
APPLICANT: Ward, Michael
APPLICANT: Penttila, Merja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10197294A
Publication No. US20030104546A1
GENERAL INFORMATION:
APPLICANT: Swanson, Barbara A.
APPLICANT: Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 223; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Saloheimo, Markku
TITLE OF INVENTION: Microbial Swollenin Protein, DNA
TITLE OF INVENTION: Such Swollenins
TITLE OF INVENTION: Such Swollenins
FILE REFERENCE: GC378-2-D1
CURRENT APPLICATION NUMBER: US/10/197,294A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 09/112,498
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 08/893,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penttila, Merja
APPLICANT: Pere, Jaakko
APPLICANT: Saloheimo, Markku
                                                                                                                                                                                              179
                                                                                                                                                                                                                                204
                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                           144 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
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                                                                                                                                                                                                                    QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                                                                                                                                                                                                                                                                                                    TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI
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                                                                                                                                                                                                                                                                       VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQAMSRNWG
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98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1228; DB 15;
Pred. No. 1.2e-114;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Method
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APPLICANT: Pere, Jaakko

APPLICANT: Saloheimo, Markku

ITITLE OF INVENTION: Microbial Swollenin Protein, DNA

ITITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing

ITITLE OF INVENTION: Such Swollenins

ITITLE OF INVENTION: AUMBER: US/10/197,294A

CURRENT FILLING DATE: 1998-07-09

PRIOR FILLING DATE: 1998-07-09

PRIOR FILLING DATE: 1997-07-11

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: PastSEQ for Windows Version 4.0

CURRENTH: 223

TYPE: PRI
ORGANISM: Trichoderma reesei
                                                                                                                                                                                                                                  APPLICANT: Pere, Jaakko
APPLICANT: Saloheimo, Marku
APPLICANT: Saloheimo, Marku
TITLE OF INVENTION: Microbial Swollenin Protein, DN
TITLE OF INVENTION: Sequences Encoding Such Swolle
TITLE OF INVENTION: Such Swollenins
TITLE OF INVENTION: Such Swollenins
TILE REFERENCE: GC378-2-D1
CURRENT APPLICATION NUMBER: US/10/197,294A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 09/112,498
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 08/893,766
PRIOR FILING DATE: 1997-07-11
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                                                                              US-10-197-294A-5
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                                                                                             SEQ ID NO 5
LENGTH: 222
TYPE: PRT
ORGANISM: Plant/eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.1%;
Best Local Similarity 88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10197294A Publication No. US20030104546A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 199;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Swanson, APPLICANT: Ward, MAPPLICANT: Penttil
                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWQSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFELTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ward, Michael
Penttila, Merja
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbara A.
  79.6%;
88.0%;
                                                                                                                                                                                                    Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
     Score 1109.5; DB 15; Length Pred. No. 8.1e-103;
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Pred. No. 5.8e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Such Swollenins and Method of Producing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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Matches 198;

Conservative

16;

Mismatches

Indels

Gaps

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RESULT 6
US-10-197-294A-12
Sequence 12, Application US/10197294A
Publication No. US20030104546A1
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SEQ ID NO 4
LENGTH: 258
TYPE: PRT
ORGANISM: Gossypium hirsutum
US-10-150-559-4
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US-10-150-559-4
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Best Local S
Matches 182
                                                                                                                            GENERAL INFORMATION:
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APPLICANT: Swanson, Barbara A.
APPLICANT: Ward, Michael
APPLICANT: Penttila, Merja
APPLICANT: Pere, Jaako
APPLICANT: Saloheimo, Markku
TITLE OF INVENTION: Microbial Swollenin Protein, DNA
TITLE OF INVENTION: Sequences Encoding Such Swollenins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wilkins, Thea A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Bicengineering Cotton Fiber Properties
FILE REFERENCE: 023070-116500US
CURRENT APPLICATION NUMBER: US/10/150,559
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                         194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFFLFSICNSIFLGANGDDNGGWQTAHATFYGGADATGTMGGACGYGNLYSQGYGTSTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNDPK-CLPGSITVTATNFCPPNFALPNNNGGWCNPPLQHFDLAQPAFLKIAQYRAGIVP
                                                                                                                                                                                                                                                                                                                        VSIKGSKTGWLPMSRNWGQNWQSNAYLNGQSLSFKVTASDSRTITNYNVVPAGWQFGQTF
                                                                                                                                                                                                                                                                                                                                                VSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTY 245
                                                                                                                                                                                                                                                                                                                                                                                             FDLAEPAFLQIAEYRAGIVPVMFRRVSCVKKGGIRYTMNGHSYFNMVLITNVGGAGDITS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSTALFUNGLSCGAFYELRCUNDPOWCISRTITVTATUFCPPNYALSSDNGGWCNPPREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                                                                                                                                                                                                                       EGPQF 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFFVFTFA-----DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.9%; Score 1044; DB 12; 74.3%; Pred. No. 3.4e-96; tive 27; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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   and Method of Producing
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                                                                                                                                                                                                               ; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 9
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Zea mays
US-10-409-701-9
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US-10-409-701-9
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Publication No. US20030221224A1
                                                                                                                                             Matches
                                                                                                                                                          Ouery Match
Best Local S
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                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/370,796
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1421
CURRENT APPLICATION NUMBER: US/10/409,701
CURRENT FILING DATE: 2003-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zinselmeier, Chris
APPLICANT: Helentjaris, Timothy G.
TITLE OF INVENTION: Enhanced Silk Exsertion Under
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                                                                                                                                                          Similarity
                      TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHPDMAEPAFLQIAQYRAGI 143
                                                                     RCDNNGQSCLPGTITVTATNFCPPNYGLPSDDGGWCNPPRPHFDMAQPAFLQIAQYRAGI
                                                                                                                                             Conservative
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185

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73.7%; Score 1027; DB 12; 78.0%; Pred. No. 1.7e-94; 75. Mismatches 25;

Length

253; 0

Indels

Gaps

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86 83 4.0

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; LENGTH: 233;
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
; FEATURE:
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(233)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-197-294A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/197,294A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 09/112,498
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 08/893,766
PRIOR PILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Such Swollening FILE REFERENCE: GC378-2-D1
                       203 GQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                                                                                                                                                                                                                                23 ADYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFE
                                                                                                                                                                             IVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNW 202
                                                                                         IVPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNW
                                                                                                                                                                                                                                                                         ADYGSWQSAHATFYGGGDASGTMGGACGYGNLYSTGYGTNTAALSTVLFNDGAACRSCYE 65
GONWOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGWQFXQTFEGGQF
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                                                                                                                                                                                                                                                                                                                                                                                       74.2%;
78.1%;
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Pred. No. 2.4e-95;
23; Mismatches 27;
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US-09-896-301-2
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                                                                                                               RESULT 9
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PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
PRIOR FILING DATE: 1993-05-12
PRIOR FILING DATE: 1993-05-12
PRIOR FILING DATE: 1993-05-12
NUMBER: 0F SEQ ID NOS: 7
Sequence 8, Application US/10197294A Publication No. US20030104546A1 GENERAL INFORMATION: APPLICANT: Swanson, Barbara A. APPLICANT: Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09896301
Patent No. US20020103355A1
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
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TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE
LOCATION: 211
OTHER INFORMATION: Xaa is unknown or other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: rice expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                          146 VSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN
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                                                                                                                                                                                                                                          VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN
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APPLICANT: Penttila, Merja
APPLICANT: Pere, Jaakko
APPLICANT: Saloheimo, Markku
TITLE OF INVENTION: Microbial Swollenin Protein, DNA
TITLE OF INVENTION: Sequences Encoding Such Swollenins
TITLE OF INVENTION: Sech Swollenins
TITLE OF INVENTION: Such Swollenins
TITLE OF INVENTION Such Swollenins
FILE REFERENCE: GC378-2-D1
CURRENT APPLICATION NUMBER: US/09/112,498
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US/08/893,766
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US-10-197-294A-9
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                                                                                          US-10-197-294A-9
                                                                                                                                    SEQ ID NO 9
LENGTH: 232
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10197294A Publication No. US20030104546A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 8
LENGTH: 236
Query Match
Best Local Similarity
Matches 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pere, Jaakko
APPLICANT: Saloheimo, Markku
TITLE OF INVENTION: Microbial Swollenin Protein,
TITLE OF INVENTION: Sequences Encoding Such Swo
TITLE OF INVENTION: Such Swollenins
FILE REFERENCE: GC378-2-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Swanson, Barbara A. APPLICANT: Ward, Michael
                                                                                                                                                                                                      PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                  ORGANISM: Plant/eukaryotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQPGQTYEGPQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 QNDGKWC-PGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP
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  72.7%;
ilarity 77.6%;
Conservative 2:
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78.6%;
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  Score 1013.5; DB 15;
pred. No. 3.4e-93;
5; Mismatches 25; I
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09896301 Patent No. US20020103355A1
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                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin -09-896-301-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cosgrove, Daniel APPLICANT: McQueen-Mason,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                    Similarity
                    QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
                                                                                                    VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG 203
                                                                                                                                                      RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI
                                                                                                                                                                              TCTNDFKWCLFGTIRVTATNFCFPNFALPNNNGGWCNFFLQHFDMAEFAFLQIAQYRAGI 143
                                                                                                                                                                                                                                                                         DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 83
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                                                                         VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVINVAGPGDVQSVSIKGSSTGWQPMSRNWG
                                                                                                                                                                                                                                    DYSSWOSAHATEYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 232
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QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF
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Guiltinan, Mark J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shcherban, Tatyana
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                  72.6%; Score 1011.5; DB 10; 77.1%; Pred. No. 5.2e-93; 1: ive 23; Mismatches 28; I:
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                                                                                                                                                                                                                                                                                                                                                       Length
226
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RESULT 12

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APPLICANT: Swanson, Barbara A.

APPLICANT: Ward, Michael

APPLICANT: Penttila, Merja

APPLICANT: Perty Jaakko

APPLICANT: Pere, Jaakko

APPLICANT: Saloheimo, Markku

TITLE OF INVENTION: Microbial Swollenin Protein, DNJ

TITLE OF INVENTION: Sequences Encoding Such Swoller

TITLE OF INVENTION: Such Swollenins

FILE REFERENCE: GC378-2-D1

CURRENT APPLICATION NUMBER: US/10/197,294A

CURRENT FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 09/112,498

PRIOR APPLICATION NUMBER: US 08/893,766

PRIOR APPLICATION NUMBER: US 08/893,766

PRIOR APPLICATION NUMBER: US 08/893,766
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US-10-197-294A-11
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TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
PRIOR SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10197294A Publication No. US20030104546A1 GENERAL INFORMATION:
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
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Pred. No. 4.6e-88;
6: Mismatches 27;
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; SOFTWARE: FASTSEQ for Windows Version
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANIZM: Plant/eukaryotic
US-10-197-294A-11
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Best Local Similarity 71.4
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 237
                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/10197294A Publication No. US20030104546A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: GC378-2-D1
CURRENT APPLICATION NUMBER: US/10/197,294A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 09/112,498
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Saloheimo, Markku
TITLE OF INVENTION: Microbial Swollenin Protein, DNA
TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
TITLE OF INVENTION: Such Swollenins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Swanson, APPLICANT: Ward, M
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/893,766 PRIOR FILING DATE: 1997-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                  ORGANISM: Plant/eukaryotic 10-197-294A-14
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 129
                       144 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                         69
                                                                                                                                                                                                                         cch 67.2%; Score 937; DB 15; al Similarity 72.7%; Pred. No. 1.5e-85; 165; Conservative 21; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
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                                                                                                  86 TNDPKWCLPG--TIRVTATNPCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI
                                                                                                                                                                                    26 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
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                                                                                                                                             GPWTSAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKC
 VPVAYRRVPCRKAGGIRFTINGFRYFNLVLITNVAGAGDIVRVSVKGTNTAMMTMSRNWG
                                                                         DODPRWCNPGNPSILITATNFCPPNFAEPSDNGGWCNPPRPHFDLAMPMFLKIAQYRAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNWQSNSVLVGQSLSFRVTSSDRRSSTSWNIAPANWKFGQTFMGKNF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penttila, Merja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pere, Jaakko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.4%; Score 940; DB 15; 71.4%; Pred. No. 7.8e-86;
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Search completed: December 18, Job time : 32 secs

2003, 17:55:20

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Publication No. US20030104546A1
GENERAL INFORMATION:
APPLICANT: Swanson, Barbara A.
APPLICANT: Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/112,498
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 08/893,766
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GC378-2-D1
CURRENT APPLICATION NUMBER: US/10/197,294A
CURRENT FILING DATE: 2002-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Microbial Swollenin Protein, TITLE OF INVENTION: Sequences Encoding Such SwoTITLE OF INVENTION: Such Swollenins
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 233
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                                                                                                                                                       74 VNDPQWCIKGRSIVVTATNFCPP-----GGACDPPNHHFDLSQPIYEKIALYKSGII
NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
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                                                                              PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ
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Penttila, Merja
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                                                                                                                                                                                                                                                                                                      63.8%; Score 889.5; DB 15; 69.5%; Pred. No. 8.4e-81; ative 26; Mismatches 34;
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPT0_sol_p/US09383579/runat_18122003_171927_28772/app_query.fasta_1.391
-Q=/cgn2_1/USPT0_sol_p/US09383579/runat_18122003_171927_28772/app_query.fasta_1.391
-DB=GenEmbl -OEMT=fastap_-SUFFIX=rye -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US09383579_@CGN 1_1 4958 @runat_18122003 171927_28772 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADSI -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXI=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
          December 18, 2003, 22:33:47; Search time 2802 Seconds (without alignments) 3650.038 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

## ð 1275 1275 1275 1275 1160.5 1152.5 1151.5 1151.5 1143.5 1141 1105 1102.5 1102.5 1101.5 1100 1100 1092 1092 1092 1095 1085 1085 1085 1077 1076.5 1077 1076.5 1077 1076.5 1077 1078.5 1138 1133.5 1133.5 1130.5 1125 1126 1116.5 11116.5 1113.5 1113.5 1113.5 Score Query Match Length 996 681 11048 11049 11049 11049 11142 11143 11143 11143 111443 111443 111443 111443 111443 111443 111443 111443 111443 111443 111443 111443 111443 111443 DB AF159563 AF3150936 AF3150936 AY079208 AY079208 AY0792083 AB029083 AF028175 AF038815 AF085330 AB1044445 AX306490 PAU93167 CAR291817 PTU64891 AY299692 CAR489608 AB104442 AB093029 AB093030 AF049354 AF096776 AB104444 AB093028 AB104443 AF297521 AX306492 CSU30382 Ä AR161478 U93167 Prunus arme AJ29151 Prunus av AF297521 Prunus av AF297521 Prunus ce AF23033 Prunus ce AF23033 Prunus ce AF350937 Prunus ce AF350937 Prunus com AB104444 Vitis lab AB093028 Pyrus com AB093030 Pyrus com AB093030 Pyrus com AB093030 Pyrus com AF026174 Rumex pal AF067676 Malus x d AF049354 Nicotiana AF159563 Fragaria AF167360 Rumex pal AF079206 Mirabilis AY079206 Mirabilis AY079208 Mirabilis AY079208 Mirabilis AY079208 Prunus pe AY079208 Mirabilis AY079208 Prunus pe AY079208 Mirabilis AY079208 Wirabilis AY079208 Virius taeda AF04891 Pinus taeda AY299692 Sambucus U64891 Pinus taeda AY299692 Sambucus U64891 Pinus taeda AX506393 Sequence U64893 Pinus taeda AY086770 Arabidops U64892 Pinus taeda AY079205 Mirabilis AX392019 Sequence AJ489608 Cicer ari AB104442 Vitis lab AB093031 Pyrus com AB093032 Pyrus com AR076514 Sequence AR161478 Sequence AX306492 Sequence AX306490 Sequence Description U30382 Cucumis

ALIGNMENTS

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Best Local Si
Query Match:
DB:
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ORIGIN
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AUTHORS
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Pred. No.:
                                                US-09-383-579C-10 (1-250) x CSU30382
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MEDLINE
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 154
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Shcherban, T.Y., Shi, J., Durachko, D.M., Guiltinan, M.J.,
McQueen Mason, S.J., Shieh, M. and Cosgrove, D.J.
Molecular cloning and sequence analysis of expansins—a highly
conserved, multigene family of proteins that mediate cell wall
extension in plants
Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)
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Cucumis sativus expansin
U30382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania
State University, 208 Mueller Laboratory, University Park, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 992)
Shcherban, T., Shi, J., Durachko, D.M., Guiltinan, M.J.,
McQueen-Mason, S.J., Shieh, M. and Cosgrove, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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             MetAlaPheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePhePheValPhe
 ATGGCTTTTTCTTACTCACCCTTCTCCTCTCTCTTTCTTCTTTCTTTCTTTCTTTCTTCTTC
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                                                                                                                                                                                                                                                                                                 /translation="MAFSYSPESSLELLPFFFVETFADYGGWQSGHATFYGGGDASGT WGGACGYGNLYSQGYGTNTVALSTALFNNGLSCACFEMTCTNDDFWCLDGTIRVTAT NFCPPNFALPNNNGGMCNPPLQHFDWAEPAFLQIAQYRAGIVPVSFRRVPCMKXGGVR FTINGHSYFNLYLITNVGGAGDVHSVSIKGSRTCWQSMSRNWGQNWQSNNYLNGQCLS FQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF"
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Cg-EXP1"
/note="similar to pollen allergen Lol pI, Lolium perenne,
Swiss-Prot Accession Number P14946; former gene name
CuExS1; expansin-29 (Ex29) protein"
                                                                                                                                                                                            /gene="Cs-EXP1"
/note="17 A nucleotides"
277 c 177 g 279
                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="expansin_S1 precursor"
/protein_id="AAB37746.1"
/db_xref="GI:1040875"
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/mol_type="mRNA"
/strain="Burpee Pickler"
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/function="induces
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Percent Similarity:
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1 (bases 1 to 681)

Cosgrove,D.J., McQueen-Mason,S., Guiltinan,M.,
                                                                                                                                                                                                                                                                                           Unknown
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                                                                                                                                                                              Proteins catalyzing the extension of Patent: US 5959082-A 1 28-SEP-1999;
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                                         Unclassified.

1 (bases 1 to 681)

1 (bases 1 to 681)

Cosgrove,D.J., McQueen-Mason,S., Guilt Shi,J.

Purified plant expansion proteins and Patent: US 625466-A 1 03-JUL-2001;

Location/Qualifiers
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Cucumis sativus (cucumber)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                          HisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsnTrpGly
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 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln
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Location/Qualifiers
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Prunus armeniaca expansin (PA-Expl) mRNA,
U93167
U93167.1 GI:3510537
                                                                                                                                                                                                                         Submitted (12-DEC-1997) Station Vegetaux, INRA, Site AGROPARC, I Sequence update by submitter
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                              Submitted (12-MAR-1997) Station
                                                                                                                                                                                                                                                                                                                                                                            from
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                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                      Mbeguie-A-Mbeguie,D.,
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Prunus armeniaca
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                                                                                                                                                               strain="Bergeron"
                                                                                                                                                                                      organism="Prunus armeniaca"
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_stage="ripe fruit"
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VTATNFCPONFAQSNDNGGWCNPPLQHFDLAEPAFLQINQYRAGIVPVTTRRVPCMKK
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a 254 c 242 g 312 t
4.92e-104
1160.50
88.40%
82.40%
83.25%
Length:
Matches:
Conservative:
Mismatches:
Indels:
             1109
206
15
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Gaps:

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                                                                                                                                                                             GTGACCACCAGTGACGGAAGAACTGTTACAAGCTACAACGTGGCCCCTGGTAATTGGCAG
                                                                                                                                                                                                                  ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGln
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                                                                                                    TTTGGTCAGACTTTCTCAGGGGGTCAATTT
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Cicer arietinum
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                     MetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThrAlaThr 102
                                                                                                                                                             GlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsn
                                                                                                                                                                                                              GCTGATTATGGTGGTTGGGAGGGTGCTCATGCCACTTTCTATGGTGGGGGGTGATGCTTCT 185
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TCCATTGTTCTAAAGGGTCTAATTTTTTTAATTTTTTTAACATGAATATGCAAAGTGCTATA 125
ATGAGATGCAATGATCCAAGATGGTGCAAACCTGGCTCTATTATTGTTACTGCCACA
                                                                 ACAGCAGCACTAAGCACTGCTTTATTCAACAATGGTTTAAGTTGTGGATCTTGCTATGAA 305
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                                                                                         ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlu
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/clone_Tib="CAN-5"
/dev_stage="5 days old seedling"
/country="Spain"
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/mol type="mRNA"
/cultivar="Castellana"
/db_xref="taxon:3827"
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/gene="Exp1" 81. 845 /gene="Exp1" /gene="Exp1" /note="PruavExp1" /codon_start=1 /protein_id="Axc13982.1" /protein_id="Axc13982.1" /protein_id="Axc13982.1" /db_xref="GI:10180017" /translation="MARQALSIAPLALSILVLENLHLHGAFADYGGWEGAHATFYGGGD /translation="MARQALSIAPLALSILVLENLHLHGAFADYGGWEGAHATFYGGGD ASGTMGGACGYGNLYSGGYGTNTAALSTALFNNGLSCGSCYEMRCNNDFRWCRPGSII VTATNFCEPAPFAGSNNNGGWCMPFLOHFDLAEPAFLQIAQYRAGIVEVTFRRVECMKK GGIRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQFMSRNWGQNWQSNTYLNG	Columbia VOH 1ZO, Canada Location/Qualifiers 1. 1048 /organism="Prunus avium" /mol type="mRNA" /db xref="taxon:42229" 1. 1048	Cherry (Prunus avium L.) Unpublished 2 (bases 1 to 1048) 2 (bases 5 to 1048) Wu,Z. and Wiersma,P.A. Direct Submission Submitted (18-XUG-2000) J Agri-Food Research Centre	Prunus avium (sweet cherry)  Prunus avium Eukaryota; Viridiplantae; Streptophyta Spermatophyta; Magnoliophyta; eudicoty rosids; eurosids 1; Rosales; Rosaceae; 1 (bases 1 to 1048) Wu,Z. and Wiersma,P.A. Differential Expression of Expansin Ge	AF297521 1048 bp mRNA linear PLN 17-SEP-2000 N Prunus avium expansin 1 (Expl) mRNA, complete cds. AF297521 AF297521.1 GI:10180016	243 GlnThrTyrGluGlyProGlnPhe 250       ::::::   	223 LeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGly 242	203 GlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThr 222	183 ValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsnTrp 202	163 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAsp 182	143 IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr 162	123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly 142	103 ABRPHECYBProProAsRPHEALALEUProAsRASRASRGIYGIYTrpCysAsRPProPro 122

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YOO, The Contini, C., Loescher, W. and van Nocker, S.
YOO, Cander, C., Cantini, C., Loescher, W. and van Nocker, S.
Coordinated expression of genes encoding expansins and other cell
wall-modifying enzymes is associated with pectin-related changes
the cell wall during ripening of cherry (P. cerasus) fruit
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Submitted (19-FEB-2001) Department of Horticulture, Michigan St
University, 392A Plant and Soil Science Building, East Lansing,
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                             AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsn
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GGIRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTWQPMSRNWGQNWQSNTYLNG
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/db_xref="taxon:140311"
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/note="sour cherry"
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Submitted (02-FEB-2000) Biology,
Chapel Hill, NC 27599, USA
Location/Qualifiers
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Zinnia elegans
Zinnia elegans
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
Asteridae; Zinnia.
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Zinnia elegans expansin
AF230332
AF230332.1 GI:7025492
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                                                         /codon_start=1
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HSYFNLILITNVGGAGDVHSVSIKGSKTGWQSMSRNWGQNWQSNSYLNGQSLSFQVTT
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Vitis labrusca x Vitis vinifera
Vitis labrusca x Vitis vinifera
Vitis labrusca x Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
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89.20%
81.20%
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PheGlyGlnThrTyrGluGlyProGlnPhe 250
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Exoression of Expansin ge
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                                                                    IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGly
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42. .800
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School of Natural Science and Technology;
Okayama, Okayama 700-8530, Japan
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Hiwasa, K., Kubo, Y., Nakano, R. and
Direct Submission
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                          LeuValProSerAsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe
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Submitted (21-FEB-2003) Megumi Ishimaru, Osaka
University, Graduate School of Agriculture and
1-1, Gakuen-cho, Sakai, Osaka 599-8531, Japan
(B-mail:m_ishima@plant.osakafu-u.ac.jp, Tel:81-
Fax:81-72-254-9418)
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Vitis labrusca x Vitis vinifera
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids; Vitaceae; Vitis.
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CysG1yA1aCysPheG1uMetThrCysThrAsnAspProLysTrpCysLeuProG1yThr
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                         Hiwasa,K., Kubo,Y., Nakano,R. and Inaba,A. Direct Submission Submitted (08-0CT-2002) Kyoko Hiwasa, Okayama University, School of Natural Science and Technology; Tsushima-naka 1. Okayama, Okaya
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/dev_stage="ripening fruit"
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/db_xref="taxon:23211"
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                                                                                   MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeu
                                                                                                                                                                                                                                                                                                                                              TrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
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                  SerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSer 237
                                                                                                                                                        GlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSer
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                                                                                                                                                                                                                                                                           CAATACAGAGCTGGAATTGTCCCCCATCTCCTTCAGAAGGGTTTCGTGTGAAGAAGGGA
                                                                                                                                                                                                                                                                                                 GlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGly
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AB093030
LOCUS
DEFINITION
ACCESSION
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146 GTATTTGCTGTTTATGGTAGCTGGGAAGGCGCTCATGCCACATTTTACGGTGGCGGTGAT 205
                      21 ThrPheAlaAspTyrGlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyAsp
                                                                        98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-OCT-2002) Kyoko Hiwasa, Okayama University, Graduate School of Natural Science and Technology; Tsushima-naka 1-1-1, Okayama, Okayama 700-8530, Japan (B-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:81-86-251-8338, Fax:81-86-251-8338)
                                                                                          2 AlaPheSerTyrSerProPheSer---SerLeuPheLeuLeuProPhePhePheValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiwasa,K., Rose,J.K., Nakano,R., Inaba,A. and Kubo,Y. Differential expression of seven alpha-expansin genes during and ripening of pear fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB093030 1118 bp
Pyrus communis PcExp3 mRNA for 6
AB093030
AB093030.1 GI:29467502
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Hiwasa,K., Kubo,Y., Nakano,R. and Inaba,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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41 AlaSerGlyThrmerGlyGlyAlacysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly	ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGln	•	
41 AlaSerGlyThrmerGlyGlyAlacysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly		•	
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41 AlaSerGlyThrmerGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly	GlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArg		
41 AlaserGlyThrWetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly [		•	
41 AlaSerGlyThrMerGlyGlyAlacysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly	PheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuTleThrAsnValGlyGlyAla	·	
41 AlaSerGlyThrmetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly	GCTGGAATCGTGCCGGTTTCCTTCAGAAGAGTACCTTGTGTGAAGAAAGGAGGAATAAGA	•	
41 AlaSerGlyThrmetGlyGlyAlaCysGlyTyrGlyAsnieuTyrSerGlnGlyTyrGly	AlaGlyIleValProValSerPheArgArgValProCysMetLysGlyGlyValArg		
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41 AlaserGlyThrMetGlyGlyAlaCysGlyTlyrGlyAsnLeuTyrSerGlnGlyTlyrGly	ACCAACACTGCAGCTTTGAGCACAGCATTGTTCAACAATGGCTTAAGCTGTGGGTCTTGT		
41 AlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly	ThrasnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCys	,	
41 AlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGly	GCTTCTGGCACAATGGGAGGAGCATGTGGTTATGGGAATTTGTACAGCCAGGGGTATGGA	•	
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Job time : 2807 secs

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pr printed,

> and is derived by analysis of the total score distribution

## Result No. 1085 1071.5 1041 1041 1041 1041 1036.5 1024. 928 919.5 919.5 989.5 889.5 870 857.5 836.5 836.5 831 795 Score 1275 1275 1275 1275 Query Match Length 1144 780 1198 1233 753 687 1324 1326 1015 88 AAZ93526 AAC41531 AAV68447 A AAC34714 AAD03711 AAT30268 AAT13053 AAT70039 AAC45165 AAD03713 AAC41263 AAD03712 ABZ12286 ABA97164 AAT13320 ABA97162 AAC38981 AAV68446 ABN98723 AAD32963 ABZ12284 ABZ13264 AAD32964 ABA97161 SUMMARIES Arabidopsis thalia Pear expansin 2 (E Arabidopsis thalia Cotton fibre clone Cotton fibre-speci Cotton B12 gene an Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Tomato seed expans Arabidopsis thalia Tomato expansin Le Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Pear expansin 1 (E Arabidopsis thalia Arabidopsis thalia Description Tomato seed expans Arabidopsis thalia Arabidopsis thalia Cucumber expansin-C. sativus DNA enc C. sativus DNA enc Expansin gene sequ Arabidopsis thalia Expansin gene sequ Arabidopsis thalia Arabidopsis thalia Tomato seed expans Arabidopsis thalia Melon expansin CmE Arabidopsis thalia

ALIGNMENTS

RESULT 1 AAT13320 Expansin-29; plant cell wall; cellulose; paper recycling; de-inking; polysaccharide; cucumber; ss. Cucumber expansin-29 cDNA 25-MAR-2003 08-JUL-1996 AU9540262-A. Cucumis sativus AAT13320; AAT13320 standard; DNA; 681 BP. (updated)
(first entry) var. Burpee Pickler

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Percent Similarity:
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12-MAY-1995;
12-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expansin proteins which alter the mechanical strength poly:saccharide(s) - useful in paper mfr. and recycli
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                                                                 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle
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 GTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTTACAATC
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       This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of extensins possible. This sequence encodes the Cucumis sativus (cucumber) extensin, csexpla, described in
                                                                                                                                                             Vector encoding an expansin, useful in treatment of cellulosic materials for paper recycling, providing large-scale production
                                                                                                                                        Claim 2;
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                                                                                                                                      Page 14-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln
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                                      C. sativus DNA encoding S1 expansin homologue.
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                                                                                                                                                                                                                                                                                 GlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of extensins possible. This sequence encodes the Cucumis sativus (cucumber) S1 extensin homologue described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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P-PSDB; AAG80768.
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                  The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the
                                                                                                                                                                                                                                                                          Identifying a stress and producing plants
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26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
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production of transgenic plants, cells and seeds and in producing plants
                                                                                                                                                                                                          Claim 144;
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                                     with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
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Sequence 762 BP; 202 A; 196 Ç 184 <u>ი</u> 180 Η. 0 other;

Alignment S Pred. No.:

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Best Local S Query Match:

Percent Similarity: Best Local Similarity:

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GlyGlnThrTyrGluGlyProGlnPhe
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                                                                                                                                                 GTACACGCCGTCTCAATCAAAGGCTCAAAAACACAGTCGTGGCAAGCGATGTCTAGAAAC
                                                                                                                                                                                                 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAsp
                                                                                                                                                                                                                                                  ATTGTTCCTGTCTCTTTCCGAAGAGTACCATGTATGAAGAAAGGAGGAATAAGGTTTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerTyrSerProPheSerSerLeuPheLeuLeuProPhePhePheVal----PheThrPhe
                                                 ACGACCAGCGATGGTCGCACACTCGTTAGCAACGACGTGGCTCCTACTAGCAGTTG
                                                                       ThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPhe
                                                                                                            TrpG1yG1nAsnTrpG1nSerAsnAsnTyrLeuAsnG1yG1nG1yLeuSerPheG1nVa1
                                                                                                                                                                                                                                                               IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr
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                                     TCATACTTAAAATATTCAATAATCTCAATTATATCCGTATTATTCCTCCAAGGAACTCAT
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99US-0121825.

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99US-01235788.

99US-0125788.

99US-0126264.

99US-0126785.

99US-0127462.
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Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                     Arabidopsis thaliana DNA fragment
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                                                                                                                                                                                                                                                                                                                                                  IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr
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                                                                                                                                                                                                                                             ACGACCAGCGATGGTCGCACACTCGTTAGCAACGACGTGGCTCCTTCTAATTGGCAGTTC
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LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly
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                                                                                               IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr
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                           New beta-galactosidase, pectin methylesterase, polygalacturonase expansin1, and expansin2 proteins and nucleic acids, useful for regulating fruit ripening or creating transgenic plants -
         Claim 14; Page 38-39; 45pp;
                                                                   WPI; 2002-280942/32.
P-PSDB; AAE20571, AAE20578.
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                                                                                                                                                                 20-AUG-2001; 2001WO-PT00021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; cell wall hydrolase; beta-galactosidase; pectin methylesterase; beta-Gal; polygalacturonase; PG; expansin1; Exp1; expansin2; Exp2; tripening; gene expression; transgenic plant; transgenic; enzyme;
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/product= "Pear expansin 2 protein #1"
/transl_except= (pos:335..343, aa:Leu-Asn)
/transl_except= (pos:353..361, aa:Gln-Pro)
/transl_except= (pos:353..361, aa:Gln-Pro)
/transl_except= (pos:413..421, aa:Gly-Ala)
/transl_except= (pos:479..487, aa:Gly-Ala)
/transl_except= (pos:777..775, aa:Gln-Arg)
/transl_except= (pos:773..781, aa:Arg-Asn)
/transl_except= (pos:806..814, aa:Trp-Leu)
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Alignment Pred. No.: Score:

Scores:

Sequence 1144 BP;

325 A; 258

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242 G; 319

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Best I Query DB:

Percent Similarity: Best Local Similarity:

1.12e-103 1071.50 86.17% 78.66% 76.87%

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1144 199 19 30 5

US-09-383-579C-10 (1-250) x AAD32964 (1-1144)

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The present invention relates to novel genes which encode cell wall hydrolases such as beta-galactosidase (beta-Gal), pectin methylesterase (PME), polygalacturonase (PG) and cell wall proteins such as expansin1 (Exp1) and expansin2 (Exp2) proteins from pear fruit. The nucleic acids are useful for regulating fruit ripening and for suppressing endogenous beta-Gal, PME, PG, Exp1 and Exp2 genes in any fruit or other plant organs, thus modifying the structure of the cell walls of the fruit or plant and providing for ripe yet firm fruit and vegetables. The genes may be used to screen a cDNA library or a genomic library from any species, to inhibit or enhance gene expression or to produce transgenic plants. The present sequence is a cDNA encoding pear expansin 2 protein.
                                                                                                                                                                                                  rArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPh
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                                                        CCAAGTCACCACCAGTGACGGTAGAACCGTCACGAGCTACAACGTCGCGCCTGGTAATTG
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99US-0130419
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99US-0131449
99US-0132484
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pGlnPheGlyGlnThrTyrGluGlyProGln 249

8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 100-1999;

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Alignment Scores:
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99US-0139763.
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2-JUN-1999; 3-JUN-1999; 3-JUN-1999; 4-JUN-1999;

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2.13e-100
Length:
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28-FEB-2002 WO200216655-A2 Arabidopsis thaliana Arabidopsis thaliana stress regulated gene SEQ ID NO

Arabidopsis thaliana; plant; gene; stress; transgenic; ds

21-JAN-2003

(first entry)

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26-JAN-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying a stress condition to which a plan cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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This invention describes a novel vector (A) comprising (i) nucleic acid (I) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for
                                                                                                                                                                                        Vector encoding an expansin, useful in treatment of cellulosic materials for paper recycling, providing large-scale production
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ing; gene; tobacco; ds.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of extensins possible. This sequence encodes the Lycopersicon esclentum (tobacco) extensin, ntexp4a, desci in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 687 BP; 183 A; 128
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                                                  AAC47530 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGlyThrMet
                                                                                                    ACTEGAGCTCAATTC
                                                                                                                         GluGlyProGlnPhe
                                                                                                                                                                                                    PheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIleValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsnProProLeuGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMetThrCys
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                                                                                                                                                                   GlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGlnThrTyr
                                                                                                                                                                                                                                                       GTTGCTGTAAAAGGATCAAGAACTGGTTGGCAACCAATGTCAAGAAACTGGGGACAAAAC
                                                                                                                                                                                                                                                                       ValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsnTrpGlyGlnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCAAATAATGCATTGCCTAACAATGCAGGGGGTTGGTGTAATCCTCCCCTTCACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAla
                                                                                                                                                    GGCCGCAGTTTGATTTCCTACAATGTTGCACCTGCTCATTGGTCTTTTGGACAGACTTAT
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07-JUN 1999
07-JUN 1999
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110-JUN 1999
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14-MAY-1999;
14-MAY-1999;
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06-MAY-1999;
07-MAY-1999;
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05-MAR-1999

09-MAR-1999

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25-MAR-1999

26-MAR-1999

01-APR-1999

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01-APR-1999

16-APR-1999

21-APR-1999

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24-MAY-1999

04-MAY-1999

05-MAY-1999
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99US-0123180.
99US-0125788.
99US-0126264.
99US-0126278.
99US-0126264.
99US-0126274.
99US-0128714.
99US-0130477.
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44 ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr
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                         TATGACGCTGGATGGGTCAATGCTCATGCTACCTTCTATGGTGGAAGTGATGCTTCAGGA
                                                                            ATGGGTCTTTTGGGAATTGCTCTGTTTTGTTTTGCTGCAATGGTGTGCTCTGTTCATGGC
                                                                                           TTCTCTCACTCTCCTCCATTAAAGCTCTGCACTTTCTCAAAGAGAATGTTCATGGGTAAG
                                                                                                                                                PheSerTyrSerPro---
                                        -GlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGly
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1026.50
79.78%
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73.64%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 14
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25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999;
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                                                                                                                                                                                                                              Arabidopsis thaliana
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                                  (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                            The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and
                                                                                                                                                                                                                                                              Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses
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26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
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                                                              GlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGly
                                                                                                                                            GCGGTTAAAGGTTCTAGAACAAGGTGGCAACAATGTCAAGAAACTGGGGACAGAACTGG
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                                                                                              CAAAGCAACAATCTCTTAAACGGTCAAGCATTGTCATTTAAGGTGACTGCTAGTGATGGT
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-Q-/G972_1/USPTO_Spool_p/US09383579/runat_18122003 171927 28806/app_query.fasta_1.391
-DB=Issued_Patents_NA_-QFMT=fastap_-SUFFIX=rni_-MINMATCH=\overline{0.1} \cdot \c
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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US-09-092-160-1
US-07-885-970A-26
US-08-298-687A-26
US-08-298-829-26
US-08-825-642-1
US-08-845-539-5
US-08-845-539-5
US-08-845-539-5
US-08-845-539-3
US-09-362-642-3
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## ALIGNMENTS

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US-08-440-517A-1
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                                                                FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
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APPLICANT:
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MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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CITY: UNIVERSITY PARK
                 STRANDEDNESS:
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TOPOLOGY:
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                               NUCLEIC ACID
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E: PENNSYLVANIA STATE UNIVERSITY
113 TECHNOLOGY CENTER
                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
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GUILTINAN, MARK;
SHCHERBAN, TATYANA;
UNKNOWN
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RESULT 2
US-09-092-160-1
VS-09-092-160-1
Sequence 1, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: COSGROVE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEIN
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-04
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EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER RILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                             GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle
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                                                                                                                                                            HisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsnTrpGly
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             ThrTyrGluGlyProGlnPhe
                                                            SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln
                                                                                                                                                CACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGC
                                                                                                                                                                                              AATGGCCACTCATACTTCAACCTCGTTTTGATCACAAACGTCGGTGGCGCAGGCGACGTC
                                                                                                                                                                                                         AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal
                                                                                                                                                                                                                                             GTCCCCGTCTCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTTACAATC
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Matches:
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US-07-885-970A-26
                                                                                                                                                           US-09-383-579C-10 (1-250) x US-07-885-970A-26 (1-2415)
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                                                                                                                                                                                                                                         Percent Similarity:
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2415 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27,386 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 21-NOV-1990
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
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CLONE: SIB12
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TOPOLOGY: linear
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                                                          AlaAspTyrGlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSer 42
                                                                                                                            PheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePhePheValPheThrPhe
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P.O. Box 2113, First Wisconsin Plaza
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              APPLICANT: John, Maliyakal E. TITLE OF INVENTION: GENETICALLY TITLE OF INVENTION: PLANTS FOR I
                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                       ADDRESSEE: Nicholas
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                              ZIP: 53701
                                                                                                                                  COUNTRY:
                                                                                                                                                   STATE:
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                                                                                                                                                                                      E: Nicholas J.
P.O. Box 2113,
                                                                                                                                  USA
                                                                                                                                                                                        Seay,
First
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US/08/298,687A

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CLASSIFICATION BUDDERS OF THE PROPERTY OF APPLICATION NUMBER: US 07/617,239 FILING DATE: 21-NOV-1990 PRIOR APPLICATION UNMBER: US 07/253,243 FILING DATE: 04-OCT-1988 APPLICATION UNMBER: US 07/253,243 FILING DATE: 04-OCT-1988 ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J. REGISTRATION UNMBER: 27,386 TELECHONE: (608) 251-5139 INFORMATION FELLEPAX: (608) 251-5139 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 2415 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORGANISM: GOSSYPIUM barbadense STRAIN: Sea Island IMMEDIATE SOURCE: LIBRARY: EMBL-SI LIBRARY: EMBL-SI LIBRARY: EMBL-SI
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                                                               GGCACAATGGGTGAGTTTCAAACTTTCAAACCATTACCTACATAAAAATCTCTAGGCTAT 960
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GGTGGTGCAATCCCCCACGAGAACACTTTGATTTGGCCGAACCGGCATTCTTGCAGATCG 1260
                                                                                                                                               AGGGTATGGAACGAGCACAGCTTTGAGCACTGCACTTTTCAACAATGGCTTGAGCTG
                                                                                                                                                                                                            nGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCy
                                                                                                                                                                                                                                                                             -----GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGl
                   lyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleA 137
                                                                                                                              CGGTGCACTGCTACGAGCTCCGGTGCAACAATGATCCTCAATGGTGCATTAGTCGAACCA 1140
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RESC US	B 8	D Qy	B 8	p Q	D Q	B &	P Q
SULT 5 S-G0-299-26 S-GQUENCE 26, Application US/08298829 Batent No. 562082 GEREAL INCORNATION: GENETICALLY ENGINEERING COTTON TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON TITLE OF INVENTION: PLANTS FOR ALTERED FIBER NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: Micholas J. Seay, Quarles & Brady STREET: P.O. Box 2113, First Wisconsin Plaza CITY: Madison STATE: Wisconsin COUNTYR: USA ZIP: 53701 COMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk COMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Microsoft Word CURRENT ASPLICATION NUMBER: US/08/298,829 FILING DATE: 19-OCT-1994 CLASSIFICATION NUMBER: US 07/885,970 PRIOR APPLICATION NUMBER:	232 TyrasnLeuValProSerasnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe 250       :::     :::	212 LeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAla 231	192 ArgThrGlyTrpGlnSerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyr 211 	172 ValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySer 191 	152 ProCysMetLysLysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeu 171	130	7 laGlmTyrArgAlaGlyIleValProValSerPheArg

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TOPOLOGY: line
MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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IMMEDIATE SOURCE:
LIBRARY: EMBL-SI
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ArgThrGlyTrpGlnSerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyr
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                                                      ValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySer 191
                                                                                         TCATGTGTGAAGAAGGAGGCATCAGGTACACCATGAATGGACATTCGTACTTCAACATG
                                                                                                         ProCysMetLysLysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeu
                                                                                                                                            CAAATCATCACACTCTTTAAGGTATGTTAAACTGTTGGGTGTTTAACCTTTTGCAGGGTG
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                                       GTGTTGATAACCAACGTGGGAGGGGCAGGGGATATAACGTCAGTGTCCATCAAGTGTTCC 1500
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APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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LOCATION: (28)..(70
OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Lycopersicon
FEATURE:
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GACAATGGTGGCTGGTAACCCTCCTCGCCCTCACTTTGACCTCGCTATGCCTATGTTT
                           AsnAsnGlyGlyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPhe 133
                                                                                                                                        GlyAlaCysPheGluMetThrCysThrAsnAspPro-----LysTrpCysLeuProGly
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                                                                                                                       GGAGCCTGTTTTGAACTTAAATGTACAAATACTCCTAATTGGAAATGGTGTCTTCCTGGA
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Best Local Similarity:
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patent No. 5929303
GENERAL INFORMATION
APPLICANT: Bennett
APPLICANT: Rose, J.
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                                                                                 Pred. No.:
                                                                                                                                  US-08-845-539-1
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, Alan B.C.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific
TITLE OF INVENTION: Expansin Genes
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                FEATURE:
                                                                                                                                             NAME/KEY: CDS
LOCATION: 28..702
OTHER INFORMATION:
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CLASSIFICATION:
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STATE: California
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                                                                                                                                                                                                                                                                         Sequence 5, Application US/08845539 Patent No. 5929303 GENERAL INFORMATION:
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                           APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific
TITLE OF INVENTION: Expansin Genes
NUMBER OF SEQUENCES: 8
                                                                                                STATE: C
                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                CITY: San Francisco
                                                                                   ZIP: 94111-3834
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Sequence 5, Application US/09362642
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APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
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LENGTH: 537 base pairs
TYPE: nucleic acid
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OTHER INFORMATION:
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SEQ ID NO 5
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GENERAL INFORMATIO
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APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 199-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IENGTH: 537
TYPE: DNA
ORGANISM: Cucumis melo
EEATURE:
NAME/KEY: CDS
LOCATION: (1)...(537)
OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
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                                                 SerArgThrGlyTrpGlnSerMetSerArgAsnTrpGlyGlnAsnTrpGln
                                                                                           TTGGTGTTAATCACCAACGTCGCGGGTGCAGGGGATATCGTGAGGGTCAGCGTAAAAGGA
                                                                                                                  LeuValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSerValSerIleLysGly
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79.10%
57.17%
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Matches:
Conservative:
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US-08-845-539-3

Sequence 3, Application US/08845539 Patent No. 5929303 GENERAL INFORMATION:

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/845
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 0230
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0200
TELEPAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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LOCATION: 1..501
OTHER INFORMATION:
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CITY: San Francisco
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AlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArg
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                                                                                     ProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArg
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                                                      CCTCCCCGGACCCACTTGGACCTTCGCCATGCCCATGTTCTCAAGATCGCCGAGTACAAA
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Mismatches:
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Matches:
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Alignment
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; LOCATION: (1)..(501
; OTHER INFORMATION:
US-09-362-642-3
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US-09-362-642-3
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Best Local Similarity:
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APPLICANT: Bennett
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LENGTH: 501
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APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
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                 AlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArg
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                                                                                                                                       AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsn
                                                                                                                                                                                   ATCAAGTGCGGCGACGACCCAAGGTGGTGCACTGCCGGAAAGCCCTCCATTTTCGTCACC
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                                                           CCTCCCCGGACCCACTTGGACCTTCGCCATGCCCATGTTCTCAAGATCGCCGAGTACAAA
                                                                           ProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArg
                                                                                                                                                                                                                                                                                                         GGAACCATGGGGGGGTGCTTGTGGATATGGAAACCTCTACAGCCAGGGCTACGGAGTCAAC
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Matches:
Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (608) 283-247
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
TELEPAX: (608) 251-5139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
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                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: John, Maliyakal E. TITLE OF INVENTION: GENETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                    MBLL.
LIBRARY: CL.
                                                                                                                                                                                                                                                                             STRAIN: Coker 312
STRAIN: TOKER 312
DEVELOPMENTAL STAGE: 10 of the stage of the sta
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First Wisconsin Plaza
                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08298687A Patent No. 5521078
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617
PILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 07/253
APPLICATION NUMBER: US 07/253
PILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
TELEPHONE: (608) 283-2478
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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D. Box 2113,
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INFORMATION

FOR SEQ ID NO:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-08-530-797-5
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                                                                                                                                 Sequence 5, Application US/08530797 Patent No. 5597718
              GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
APPLICANT: Unbeck, Paul F.
APPLICANT: Brill, Winston J.
TITLE OF INVENTION: GENERICALY ENGINEERED COTTON
TITLE OF INVENTION: FOR ALTERED FIBER
NUMBER OF SEQUENCES: 18
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 10 day old
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKFB10
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LENGTH: 727 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                      GCTGGTTGGCAATTCGGACAAACTTTTGAAGGAGGCCAGTTT
                                                                                                                                                                                                                                           SerAsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe
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                                                                                                                                                                                                                                                                                                               LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236
                                                                                                                                                                                                                                                                                                                                                         CCTATGTCCAGAAATTGGGGCCAAAACTGGCAGAGCAATGCTTACCTTAACGGACAAAGC
                                                                                                                                                                                                                                                                                                                                                                                       SerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGly 216
                                                                                                                                                                                                                                                                                                                                                                                                                                               ValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGln 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGCATCAGGTACACCATGAATGGACATTCGTACTTCAACATGGTGTTGATAACGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAATATCGAGCTGGAATCGTCCCTGTTATGTTCAGAAGGGTGTCATGTGTGAAGAAA
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                                                                                                                                                                                                                                                                                       CTCTCTTTTAAAGTGACTGCCAGCGATGGCAGGACTATCACAGCCTACAATGTAGTGCCT
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Mismatches:
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Best Local Similarity:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,
FILING DATE: 20-SEP-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/617,239
FILING DATE: 21-NOV-90
APPLICATION NUMBER: US 07/253,:
FILING DATE: 04-0CT-88
ATTORNEY/ACENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Gossypium hirsut
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 10 da
TISSUE TYPE: fiber cells
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGIH: 727 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: CKFB1
CLONE: B12
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MEDIUM TYPE: Diskette -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
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TOPOLOGY: linear
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OPERATING SYSTEM: Macintosh
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                  GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsn
                                                                                                                                                                                                                                                                   ATAACCGTGACAGCCACCAACTTTTGTCCACCTAACTATGCTTTATCTAGTGACAATGGC
                                                                                                                                                                                                                                                                                  IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGly 116
 GTGGGAGGGGCAGGGGATATAACGTCAGTGTCCATCAAGGGTTCCAGAACAGGATGGCTA 300
                                                                                                                                GCAGAATATCGAGCTGGAATCGTCCCTGTTATGTTCAGAAGGGTGTCATGTGTGAAGAAA
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04-OCT-88
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; CLONE: 1
US-08-298-829-6
    TELEPHONE: (608) 283-2478
TELEPAN: (608) 283-2478
TELEPAN: (608) 281-5139
JINFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: GOSSPPium hirsutum
STRANN: COKer 312
DEVELOPMENTAL STAGE: 10 day old
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKFB10
CLONE: B12
-08-298-829-6
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US-08-298-829-6
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Patent No. 5620882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/298,829
EILING DATE: 19-OCT 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/885,970
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
PRIOR APPLICATION NUMBER: US 07/253,243
PRIOR APPLICATION NUMBER: US 07/253,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J.
STREET: P.O. Box 2113,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 SerAsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe 250 ::: ||||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 GCTGGTTGGCAATTCGGACAAACTTTTGAAGGAGGCCAGTTT 462
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                                                                                                              10 day old fiber cells
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First Wisconsin Plaza
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Alignment Scores:

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237 SerAsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe 250 :::	217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236          :::	197 SerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGly 216	177 ValGlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGln 196	157 GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsn 176      :::   :::	137 AlaGlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLys 156	117 GlyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136	97 IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGly 116	US-09-383-579C-10 (1-250) x US-08-298-829-6 (1-727)	. No.: 1.39e-71 Length: 727 e: 706.00 Matches: 123 ent Similarity: 91.56% Conservative: 18 Local Similarity: 79.87% Mismatches: 13 y Match: 50.65% Indels: 0 Gaps: 0

Search completed: December 19, 2003, 01:04:20 Job time : 88 secs

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Maximum DB seq length: 200000000
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-Q=(cgn2 1)(USPTO spool p./US09383579/runat 18122003 171929 28889/app query.fasta_1.391
-DB=Published Applications NA .QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS_bits -STARR=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pot -THR MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09383579 @CCN 1 1 107 @runat 18122003 171929 28889
-NCPU=6 -ICPU=3 -NO MAAP -LARGSQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOŪT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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/ Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US0A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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## ALIGNMENTS

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US-09-896-301-1
US-09-896-301-1
Sequence 1, Application US/09896301
Sequence 1, Application US/09896301
Patent No. US20020103355A1
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR PHILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR PILING DATE: 1993-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ 1D NOS: 7
SOFTWAKE: Patentin Ver: 2.1
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TRANSGENIC PLANTS

CONTAINING

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Query Match:
DB:
US-09-938-842A-1088

Sequence 1088, Application

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
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LENGTH: 681
TYPE: DNA
ORGANISM: Artificial
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                                                                                              ACCTATGAAGGCCCTCAATTC
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                                                                                                                                                                SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1088
LENGTH: 762
TYPE: DNA
CORGANISM: Arabidopsis thaliana
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APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                         AlaAspTyrGlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSer
 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly
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                                                                                           ATCAACGGACACTCATACTTCAACCTCGTTCTGATCTCCAACGTAGGAGGAGCAGGAGAC
                                                                                                           IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAsp
                                                                                                                                                 ATTGTTCCTGTCTCTTTCCGAAGAGTACCATGTATGAAGAAAGGAGGAATAAGGTTTACG
                                                                                                                                                                IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr
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Matches:
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CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1153
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APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Bioengineering Cotton Fiber Properties
FILE REFERENCE: 023070-116500US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Gossypium hirsutum FEATURE:
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                                                                                                                                                                                                                                                                                                                         AlaAspTyrGlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSer 42
                                                             LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly
                                                                                                                   AsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCysAsnProPro 122
                                                                                                                                                                   MetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThrAlaThr 102
                                                                                                                                                                                                                    ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlu
                                                                                                                                                                                                                                                                       GlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsn 62
                                                                                                                                                    CTCCGGTGCAACAATGATCCTCAATGGTGCATTAGTCGAACCATAACCGTGACAGCCACC 376
                                                                                                                                                                                                                                                        GGCACAATGGGGGGGGGGTTGTGGTTATGGAAACCTGTACAGTCAAGGGTATGGAACGAGC
                                                                                                                                                                                                                                                                                                                                                            TTTCACTTTTCTTTCTTTCAGTATCTGCAACTCCATTTTCCTTGGTGCTAATGGA- 136
                                                                                                                                                                                                                                                                                                                                                                                  PheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePhePhePheValPheThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlnThrTyrGluGlyProGlnPhe
 ATCGTCCCTGTTATGTTCAGAAGGGTGTCATGTGTGAAGAAAGGAGGCATCAGGTACACC
                     IleValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThr 162
                                                                                                  AACTTTTGTCCCCCTAACTATGCTTTATCTAGTGACAATGGCGGGTGGTGCAATCCCCCA
                                                                                                                                                                                                       ACAGCAGCTTTGAGCACTGCACTTTTCAACAATGGCTTGAGCTGCGGTGCCTTCTACGAG.
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLAN
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
I SEQ ID NO 91
                                                                                                                                                                                                                                                                                                                                                     US-09-383-579C-10 (1-250) x US-09-938-842A-91 (1-753)
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Arabidopsis
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                         64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
                                                                                                                                                                                                                                                                                                         13 LeuLeuProPhePhePheValPheThrPheAlaAspTyr-----
GCGGCGCTAAGCACGGCTCTATTCAATAATGGTCTAAGT
                                                                                                             ThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr
                                                                                                                                                                         GCCGGAGGAGGTTGGGTCAACGCACACGCCACATTCTACGGTGGTGGTGATGCTTCCGGC 126
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Sequence 8, Application US/10409701
Publication No. US20030221224A1
GENERAL INFORMATION:
APPLICANT: Zinselmeier, Chris
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Helentjaris, Timothy G.
FILE REFERENCE: 1421
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US/10/409,701
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,796
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ. ID NOS: 26
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 759
TYPE: DNA
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DB:
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US-10-409-701-8
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Best Local Similarity:
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LOCATION: (1)...(759)
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                   AspTyrGlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATGTCAAAACGATGGAAAATGGTGTCTTCCTGGCTCAATTGTCGTCACAGCCACAAAC
 GACTACGGCTCGTGGCAGAGCGCCCACGCCACGTTCTACGGCGGCGGCGACGCGTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGATGGCCAAACCATTGTCTCTAACAACGTTGCTAACGCAGGCTGGTCTTTCGGCCAG
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRITIED OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT APPLICATION NUMBER: US 60/227,866
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1069
; SEQ ID NO 1069
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US-09-938-842A-1069
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                                                                                                                                                                                                                                                                                                       APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
             TYPE: DNA
ORGANISM: Arabidopsis
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Alignment Scores:

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US-09-938-842A-89
; Sequence 89, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
APPLICANT: Harper, Joeff
APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Shu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NOS: 5379
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TYPE: DNA
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                                 GlyGlnThrTyrGluGlyProGlnPhe
                                                                            ThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPhe
                                                                                                                          TrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnVal
                                                                                                                                                                         AspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsn
                                                                                                                                                                                                                          ThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGly
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                GGTCAAACCTTTGTCGGGAAGAATTTC
                                                                                                                                                             GACATCGTGAGGGCTAGTGTGAAAGGATCACGGACTGGTTGGATGAGTTTGAGCAGAAAAC
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR PRICION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang Yun
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LENGTH: 774
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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                       HisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSerArgAsnTrpGly
                                                                            AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspVal
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GTGCGGCTAGGTGTGAAAGGAACACATACTTCGTGGATGACCATGAGTCGTAACTGGGGA
                                                                                                                       GTCCCCGTCTCTTTCCGCCGAGTGCCATGCCGGAAGAGAGGAGGAATAAGGTTCACAATC
                                                                                                                                         ValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThrIle
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RESULT 9
US-09-770-445-491/c
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Query Match:
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TITLE OF INVENTION: Expressed Sequences of A;
TITLE OF INVENTION: thaliana
TITLE OF INVENTION: CONTROL OF CONTROL
TO CURRENT PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                              US-09-383-579C-10 (1-250) x US-09-770-445-491 (1-893)
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                                                                                                                                                                                                              Percent Similarity:
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SEQ ID NO 491
LENGTH: 893
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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NAME/KEY: misc feature
LOCATION: (1)...(893)
OTHER INFORMATION: n =
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol I
Price, Jennifer I
Raines, Tracy M.
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Kricker, Maja
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION NUMBER: US/09/938,842A
CURRENT FILLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1046
LENGTH: 768
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                 Percent Similarity:
Best Local Similarity:
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US-09-938-842A-1046
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      Query Match:
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                                                                                                               US-09-938-842A-1046
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Patent No. US20020160378A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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TraagCaCgGCTCTGTTCAACAATGGTTTTAGCTGTTGGTGCTTGTTTTGAGCTCAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValProValSerPheArgArgValProCysMetLysLysGlyGlyValArgPheThrIle 163
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838.50
76.83%
61.79% .
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   Length:
Matches:
Conservative:
Mismatches:
Indels:
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152
37
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                                                                                                                                                            RESULT 11
US-09-878-574-3973
; Sequence 3973, Application Us; Patent No. US20020110548A1
; PRINCE INFORMATION:
""- RVTUM, JOSEPH R
APPLICANT: Byrum, Joseph R.
APPLICANT: La ROSa, Thomas J.
APPLICANT: La ROSa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecul
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION UMBER: US/99/878,57
CURRENT FILING DATE: 2001-12-21
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR TILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3973
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Best Local Similarity:
Query Match:
DB:
                                                ; NAME/KEY: unsure
; LCCATION: (1)..(391)
COTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-E10
US-09-878-574-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-878-574-62
               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-003-Q1-B1-D9
US-09-878-574-3973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-383-579C-10 (1-250) x US-09-878-574-3973 (1-410)
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application U Patent No. US20020110548A1 GENERAL INFORMATION:
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/33,535
PRIOR FILING DATE: 199-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 62
                                                                                                                                                                                                                                                               APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                                                               TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                   FEATURE:
                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnAsnAsnGlyGlyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyr 232
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Best Local Similarity:
Query Match:
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US-09-770-791-430
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             NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 430
LENGTH: 366
TYPE: DNA
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APPLICANT: Gorlach,
APPLICANT: An, Yone
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                                                                                             APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR FILING DATE: 2000-01-27
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ORGANISM: Arabidopsis thalians
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Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                 Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                                                                    Ledford, Brooke L. Woessner, Jeffrey P. Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                   Yu, Yang
Rameaka, Joshua G.
Page, Amy
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Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                  Hoffman, Neil
Hurban, Patrick
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Ledford, Brooke L.
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Percent Similarity:
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                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Glycine n
; OTHER INFORMATION:
US-09-878-574-3468
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                                                               US-09-383-579C-10 (1-250)
                                                                                                                 Query Match:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(154018
CURRENT APPLICATION UNMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION UNMBER: 09/333,535
PRIOR PRICATION UNMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3468
LENGTH: 373
TURNS
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Patent No. US20020110548A1
GENERAL INFORMATION:
                                                                                                                                                                                 No.:
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TTTCTTCTGGGACTTTTCTACATGATCTCACATGTCAAGGGGTATGGTTTTGGAGGTTGG
                               PheLeuLeuProPhePhePheValPheThrPheAla-----AspTyrGlyGlyTrp
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 1206
LENGTH: 391
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Best Local Similarity:
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Patent No. US20020110548A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine of OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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247
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                                                                                                                               127 AACACGAACCTCCAAGGTGCCACGGCTGACTATGGTGGTGGTTGGCAGAGTGCTCATGCC
                                                                                  34 ThrPheTyrGlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsn
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TTGTATAGCCAGGGATATGGAACTGACACTGTGGCTCTAAGCACTGCTTTGTTCAACAAT
             LeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsn
                                                                                                                                                                PheThr--
                                                                                                                                                                                             CTTAGAATGGCACACAAGGAATTTTCCATTGCCCTAGTGACTCTCATTGTTCTCTTTGTC
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Result
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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1: pir1:*
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RESULT 2 T09821

expansin (clone pPtexp3) - loblolly pine (fragment)

B & B & B &	Query Ma Best Loo Matches Qy Db Qy	RESULT T10079 expans: C:Spans: C:Date C:Acces R:Shock R:Fich R:Titl A:Titl A:Titl A:Refee A:Statt A:Molee A:Ressic A:Gene C:Supes C:Gene C:Supes F:1-23 F:24-24	RESULT 45	3
181 GDVHS 181 GDVHS 181 GDVHS 181 GDVHS 181 GDVHS 241 FGQTY 241 FGQTY	250; 250; 1 M 61 I 61 I	RESULT 1 T10079 expansin S1 precursor C;Species: Cucumis sat C;Date: 16-Jul-1999 #s C;Accession: T10079 R;Shcherban, T.Y.; Shi Proc. Natl. Acad. Sci. A;Title: Molecular clo A;Reference number: Z1 A;Accession: T10079 A;Status: preliminary; A;Accession: T20079 A;Status: preliminary; A;Residues: 1-250 <shc a;cross-references:="" a;experimental="" a;gene:="" c;function:="" c;genetics:="" c;superfamily:="" domain:="" ew="" exp1="" expa<="" expansi="" f;1-23="" f;24-250="" mediate="" product:="" signal="" source:="" td=""><td>279 270 271 271 271 271 271 271 271 271 271 271</td><td>5</td></shc>	279 270 271 271 271 271 271 271 271 271 271 271	5
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GHSYENLYLITNYGGA GHSYENLYLITNYGGA DGRTLTAYNLYPSNWO               GRTLTAYNLYPSNWO	Length 250;  Indels 0; Gaps  Indels 0; Gaps	nange 21-Jul-2 .; McQueen-Mas insa highly	expansin nomolog expansin 3 - rice expansin 3 - rice expansin - upland hypothetical prot protein T12C24.10 expansin (clone p expansin for en beta-expansin [in beta-expansin [in probable beta-exp protein p1E22.6 [ allergen Ph1 pI -	; [
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submitted to the EMBL Data Library, July 1996
A;Description: Expansins are conserved in conifers and expresses A;Accession: T09821
A;Status: profits
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A;Experimental source: Clone pPtexp2; hypocotyl
C;Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
A;Experimental source: clone pPtexp3
C;Superfamily: expansion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expansin (clone pPtexp2) - loblolly pine (fragment)
C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
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A; Residues: 1-232 < HUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Pinus taeda (loblolly pine);Deties: l6-Jul-1999 #text_change 26-May-2000;Date: l6-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
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                 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ
                                                                                  PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 204
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RESULT 5
F84831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansing are conserved in conifers and expressed
                                                                                                                                                                                                                                     A;Map position: 2
C;Superfamily: expansin
                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB; AE002093;
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-253 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: F84831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A;Experimental source: clone pPtexp5
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A; Accession: T09826
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C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
                                                                                                                                                                                                                                                                                  A;Gene: At2g40610
                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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Matches 185;
                                                                                                                                                      Matches 194;
                                                                                                                                                                                              Query Match
                                                                                                                                                                          Local Similarity
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                                                                                                          SYSPESSLELLPEFFY-FTFADYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVNAVSIKGSRSGWQPMSRNWGQ
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                                                                  SYLKYSIISIISVLELQGTHGDDGGWQGGHATFYGGEDASGTMGGACGYGNLYGQGYGTN
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                                                                                                                                                      Conservative
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82.2%;
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                                                                                                                                                      Score 1085; DB 2;
Pred. No. 1.6e-84;
2; Mismatches 31
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Pred. No. 1.5e-84;
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expansin - upland cotton

C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #te:
C;Accession: T09786
R;Orford, S.J.; Timmis, J.N.
Biochim. Biophys. Acta 1398, 342-6, 1998
A;Title: Specific expression of an expansin gene durin.
A;Reference number: Z14468; MVID:9655931; PMID:9655931
A;Accession: T09786
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-258 <ORF>
A;Cross-references: EMBL:AF043284; NID:92811277; PID:9
A;Experimental source: cultivar Siokra 1-2
C;Genetics:
A;Gene: GhEX1
C;Function:
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C;Accession: T09825
R;Hutchison, K.W.;
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A; Residues: 1-232 < HUT>
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A;Description: Expansing are conserved in conifers and expres
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                                              ;Cross-references: EMBL:AF043284; NID:g2811277; PID:g2811278
;Experimental source: cultivar Siokra 1-2
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Best Local Similarity
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Pred. No. 6.9e-84;
3; Mismatches 19;
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PMID:9655931
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C;Accession: T03298
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
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Best Local Similarity
Matches 182; Conserv
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Best Local :
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                                             QTYEGPQF 250
                                                                                                       VHSVSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFG
                                                                                                                                                   LQHFDMAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGD
                                                                                                                                                                                               TAALSTVLENDGAACRSCYELRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPP
                                                                                                                                                                                                           TVALSTALFUNGLSCGACFEMTCTUDPKWCLPGTIRVTATUFCPPUFALPUNUNGGWCUPP
                                                                                                                                                                                                                                                                       SSLFLLDFFFVFTF-----ADYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTN
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                                                                           VQSVSIKGSSTGWQPMSRNWGQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFX
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74.3%;
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                                                                                                                                                                                                                                                                                                                 Score 1043; DB 2;
Pred. No. 5.7e-81;
4; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                            (creep)
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Pred. No. 1.2e-81;
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RESULT 10
T50654
                                                                                                                                                                          A;Description: induces extension C;Superfamily: expansin C;Keywords: cell wall
                                                                                                                                                                                                                                                                                                                                                                                               expansin EXP1 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T50654
R;Shcherban, T:Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.;
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Nolecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-246 < CHO>
A; Cross-references: EMBL: U85246; NID: g1815680; PIDN: AAB81662.1;
A; Cross-references: cv. Pin Gaew 56
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                                                                                                                                                                                                                              A;Gene: EXP1
C;Function:
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C;Genetics:
                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type; mRNA A;Residues: 1-237 <SHC>
                                                                                                                                                                                                                                                                                                                                                 A;Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mult A;Reference number: Z14894; MUID:96016146; PMID:7568110 A;Accession: T50654
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cho, H.T.; Kende, H.
Plant Cell 9, 1661-1671, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expansin - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000
C;Accession: T04175
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Best Local S
Matches 185
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Best Local Similarity
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                                  GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
                                                       GGWQSGHATFYGGGDASGTWGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEWTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAE
TNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP
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                                                                                                    74.0%; Score 1032; DB 79.0%; Pred. No. 4.6e-tive 23; Mismatches
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.6e-80;
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RESULT 12
C84444
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon; L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                        C; Function:
A; Description: induces extension
C; Superfamily: expansin
C; Keywords: cell wall
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A; Residues: 1-255 < SHC>
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R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, N. R;Shcherban, T.Y.; Shi, U.S.A. 92, 9245-9249, 1995
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansional control of the con
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Best Local S
Matches 184
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ce: variety Columbia
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U.S.A. 92, 9245-9249, 1995
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Pred. No. 7.3e-80;
9; Mismatches 35
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euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84820
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A;Molecule type: DNA
A;Residues: 1-248 <STO>
A;Cross-references: GB:AE002093; NID:g3461833; PIDN:AAC32927.1; GSPDB:GN00139
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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A;Map position: 2
C;Superfamily: ex
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: At2g39700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001;Accession: D84820
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                                                                                                                                    LQHFDMAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGD
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                                                                                                                                                                                                                    ALSTALFNNGLSCGACFEMTCTNDPKWCLPG--TIRVTATNFCPPNFALPNNNGGWCNPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVPV
  QTYEGPQF 250
                                                                       VHSVSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFG
                                                                                                                                                                                            ALSTALFNNGMSCGACFELKCANDPQWCHSGSPSILITATNFCPPNLAQPSDNGGWCNPP
                                                                                                                                                                                                                                                                         LFTTFVLFSLADARIPGIYSGGAWQNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTA
                                                                                                                                                                                                                                                                                                            LLPFFFVFTFADY-----GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTV
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                                    IVRASVKGSRTGWMSLSRNWGQNWQSNAVLVGQALSFRVTGSDRRTSTSWNMVPSNWQFG
                                                                                                                  REHFOLAMPVFLKIAQYRAGIVPVSYRRVPCRKRGGIRFTINGHRYFNLVLITNVAGAGD
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78.1%;
                                                                                                                                                                                                                                                                                                                                                 71.2%; Score 993; DB 2; Length 257; 71.4%; Pred. No. 9.9e-77; tive 24; Mismatches 37; Indels
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Pred. No. 2.3e-79;
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C;Accession: T07630
R;Rose, J.K.C.; Lee, H.H.; Bennett, A.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 5955-5960, 1997
Proc. Natl. Acad. Sci. U.S.A. 94, 5955-5960, 1997
A;Title: Expression of a divergent expansin gene is fruit-specific A;Reference number: Z16063; MUID:97303239; PMID:9159182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T47689
expansin-like protein - Arabidopsis thaliana
NyAlternate names: protein T22EL6.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
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R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; submitted to the Protein Sequence Database, February
                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-261 <ROS>
                                                                                                                                                                                                                                                                                                           C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change
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A; Note: T22E16.160
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A; Accession: T47689
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                                                                                                            A;Cross-references: EMBL:U82123; NID:g2062420; PIDN:AAC63088.1; A;Experimental source: cultivar Castlemart; fruit
                                                                                                                                                                                                                                                                                                                                               expansin 1 - tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: expansin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-260 <BEN>
A;Cross-references: EMB
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                                     Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 172;
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Best Local Similarity
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   Query Match
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                                                                         EXP1
                                                        specifically expressed
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                                     expansin
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8; Mismatches 45
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Search completed: Job time : 21 secs	Qy Db	D Qy	Qy dg	D Qy	g V	Best Loc Matches
Search completed: December 18, 2003, 17:50:20 Job time : 21 secs	234 LVPSNWQFGQTYEGPQF 250     :      243 MVPSHWQFGQTFIGKNF 259	174 ITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYN 233 	114 NNGGWCNPPLOHFDMAEPAFLQIAQYRAGIVÞVSFRRVÞCMKKGGVRFTINGHSYFNLVI 173                    :           :   :	58 GYGTNTVALSTALFNNGLSCGACFEMTCTINDPKWCLPGTIRVTATNFCPPNFALPN 113	13 LLPFFFVFTFADY	Best Local Similarity 65.8%; Pred. No. 4.8e-73; Matches 169; Conservative 29; Mismatches 40; Indels 19; Gaps 3;.

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Result
No.
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Maximum Match 100%
Listing first 45 s
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1394
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        SwissProt_41:*
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**RRRRRR** 

EMBL; AC002336; AAB87577.1; -.

PIR; F84831; F84831.
InterPro; IPR0071112; Expan\_Lol\_pl.
InterPro; IPR0071118; Expan\_Lol\_pl.
InterPro; IPR0071118; Expan\_Lol\_pl.
InterPro; IPR007117; Expan\_Lol\_pl.
Pfam; PF01357; Pollen\_allergen; 1.
PRINTS; PR01225; EXPANSNPAMLY.
ProDom; PD002179; Expan\_Lol\_pl\_C; 1.

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	requires a n email to	1-profit 1 this s	Bic	ROT entr	"http://www.bio.psu.edu/expansins/"	3: NAME=	TY: Con	TY: BEL	δ	ans.	g nonc	V: Causes		; id analys	., White	., Somervi	Cronin L	Ketchum	Mason T.M.,	33487; P	. Columbia;	2	; Brassı 3702:	ca; Magn	rnalian Viridipl	340610 C	sin 8 pr			STAN				8.1					15.6	•	
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1	agreement	ions as	of Bioin	copyright.	du/expa	omepage	expansin-like	E EXPAN		tic act	nding b	orande:		chromosome		ä		J.J.,	C.L.,	97			1881 Cace	eudico	eptophy		t-EXP8)	sequence v	_	PRT;		ALLIGN	YMS5 CAEEL	GUN5_TRIRE	EXER MAISE	EXB5_ARATH	EXL2 ARATH		EXL1 ARATH		
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Best Local Sim:
Matches 194;
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PROSITE;
Cell wall
SIGNAL
CHAIN
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SEQUENCE
                 Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hopper S., Lee A., Lee J.M., Lenz C.A., Li, J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Militscher J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Alpha-expansin 10 precursor (At-EXP10) (AtEX10) (Ath-ExpAlpha-1.1)
EXP10 OR ATIG26770 OR T24P13 14 OR T24P13.15.
Arabidopsis thaliana (Mouse-ear cress).
Enbryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosid
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"Altered expression of expansin modulates leaf growth abscission in Arabidopsis thaliana.",
Proc. Natl. Acad. Sci. U.S.A. 97:9783-9788(2000).
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STRAIN=cv. Columbia;
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MEDLINE=21016719; PubMed=11130712;
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VHAVSIKGSKTQSWQAMSRNWGQNWQSNSYMNDQSLSFQVTTSDGRTLVSNDVAPSNWQF
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  Salzberg S.L.,
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25 POTENTIAL.
253 ALPHA-EXPANSIN 8.
160 EXPANSIN-LIKE EG45.
250 EXPANSIN-LIKE CBD.
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160 E
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  Schwartz
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ENDGKWCLÞGSÍVYTÁTNFCÞÞNNAÍLANNNGGWCNÞÞLEHFDLAQÞVFQRÍAQYRAGIVÞ VSFRRVÞCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN

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RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

RT Sibmitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

RI Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

CC disrupting noncovalent bonding between cellulose microfibrils and cc disrupting noncovalent bonding between cellulose microfibrils and cc matrix glucans. No enzymatic activity has been found. Plays a cc major role in control of leaf growth and influences the mechanical cc preakage behavior of the pedicel.

CC -1 TISSUE SPECIFICITY: Most highly expressed in the young leaf petiole and midrib, in trichomes and at the base of the pedicel.

CC -1 DEVELOPMENTAL STAGE: Expression is first seen at the base of the cc emerging first two true leaves but not of the cyclyledons. As leaf development progresses expression begins in the base of the petiole and gradually extends toward the whole midrib and later it complete and gradually extends toward the whole midrib and later it clist is restricted to the vasculature of the petiole and leaf blade and clistoppears as the leaf matures.

CC -1 SIMILARITY: Contains 1 expansin-like CBD domain.

CC -1 DATABASE: NAME-EXPANSIN homepage;

CC -1 DATABASE: NAME-EXPANSIN homepage;
                                                                                                                   Query Match
Best Local S
Matches 179
                                                                                                                                                                                      DOMAIN
DOMAIN
SEQUENCE
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Utterback T., '
Wu D., Yu G., I
"Sequence and
                                                                                                                                                                                                                                                                         PROSITE; PS
Cell wall;
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STRAIN=cv. Col
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PRODOM; PD002179; Expan Lol_pi C;
PROSITE; PS50843; EXPANSIN_EG45; 1
PROSITE; PS50842; EXPANSIN_EG45; 1
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF229437; AAF61712.1;
EMBL; AF229431; AAF61713.1;
EMBL; AC006535; AAF87031.1;
EMBL; AY052247; AAK97717.1;
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                                                                                                                                                                                                                                                           SIGNAL
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InterPro; IPR007118; Expan_Lol_pl.
InterPro; IPR007117; Expan_Lol_pl_C.
Pfam; PF01357; Pollen_allergen; 1.
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                                                                                                                      179;
               98
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                                                                                                                                    Similarity
TNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP
                                               GGWINAHATFYGGGDASGTMGGACGYGNLYSQGYGTSTAALSTALFNNGLSCGSCFEIRC
                                                                      GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
                                                                                                                                                                                                                                                                         Signal; Multigene
                                                                                                                                                                                      166
249 l
                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n L.J., Tambunga G., Toriumi M.J., Town C.D.,
Van Aken S., Vaysberg M., Vysotskaia V.S., Walker
Fraser C.M., Venter J.C., Davis R.W.;
analysis of chromosome 1 of the plant Arabidopsis
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156
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                                                                                                                                   74.7%;
79.6%;
                                                                                                                                                                                        MW;
                                                                                                                                                                                      POTENTIAL.
ALPHA EXPANSIN 10.
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
EXPANSIN-LIKE CBD.
                                                                                                                                      Pred.
                                                                                                                                                    Score 1041;
                                                                                                                                                                                                                                                                           family
                                                                                                                      Mismatches
                                                                                                                                        No.
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                                                                                                                                    1; DB 1;
9.1e-82;
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RESULT REPORT OF THE PROPERTY 
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          맑
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28-FEB-2003 (Rel. 41, Last sequence update)
Alpha-expansin 1 precursor (At-EXP1) (Ath-ExpAlpha-1.2).
EXP1 OR AT1669530 OR F10013 18.
EXP1 OR AT1669530 OR F10013 18.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96016146; PubMed=7568110; Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J., McQueen-Mason S.J., Shieh M., Cosgrove D.J.; McQueen-Mason S.J., Shieh M., Cosgrove D.J.; Shieh M.J.; Shieh M., Cosgrove D.J.; Shieh M.J.; Shieh M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinozaki K., Davis R.W., Ecker J.R., Theol
"RIKEN Arabidopsis full length cDNA clones
SSP consortium (Salk/Stanford/PEC).";
Submitted (AUG-2001) to the EMBL/GenBank/DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARATH
                                                                                                                                                                                                                                                                                                                                                                             Durachko
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                                                                                                                                                                                                                                     "Expression patterns for selective expansin genes in Arabidopsis.";
(In) Abstracts of Plant Biology '99: The annual meeting of the American Society of Plant Physiologists, abstract#56, Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE
    similarity) SUBCELLULAR
                                      FUNCTION: Causes loosening and extensi disrupting noncovalent bonding betweer matrix glucans. No enzymatic activity similarity)
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lones (RAFLs)
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Best Local
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InterPro; IPR007118; Expan_Lol_pl_C.
InterPro; IPR007117; Expan_Lol_pl_C.
InterPro; IPR007117; Expan_Lol_pl_C.
Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNEAMLY.
PR000m; PD002179; Expan_Lol_pl_C; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
Cell_wall; Signal; Multigene_family.
      ARATH STANDARD; PRT; 255 AA. Q38866; Q9FLC5; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Alpha-expansin 2 precursor (At-EXP2) (AtEx2) EXP2 OR AT505290 OR K18123.9.
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SEQUENCE
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EMBL;
Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restropy pron-profit institutions as long as its content
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
EXPANSIN-LIKE CBD.
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AMTSH -> NSARD (IN R
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25; Mismatches
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                        (Ath-ExpAlpha-1.12).
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Query Match
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Matches 184
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J., McQueen-Mason S.J., Shieh M., Cosgrove D.J., Which M., Cosgrove D.J., Which M., Cosgrove D.J., Shieh M., Cosgrove D.J., Shieh M., Cosgrove D.J., Shieh M., Cosgrove D.J., a high conserved, multigene family of proteins that mediate cell wall extension in plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome features of the regions of 1,381,565 bp covered by twent physically assigned P1 and TAC clones.";
DNA Res. 5:131-145(1998).
-I- FUNCTION: Causes loosening and extension of plant ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U30481; AAB38073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002179; Expan_Lol_pI_C; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbi
MEDLINE=98344145;
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                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI_C.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98344145; PubMed=9679202; Kaneko T., Kotani H., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96016146; PubMed=7568110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01225; EXPANSNFAMLY.
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IR; T50656; T50656.
InterPro; IPR007112; Expan_endogl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
SUBCELLULAR LOCATION: Cell-wall bound.
SUBCELLULAR TY: BELONGS TO THE EXPANSIN FAMILY.
SIMILARITY: Contains 1 expansin-like EG45 domain.
SIMILARITY: Contains 1 expansin-like CBD domain.
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66
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                                                                                                                 FSYSPFSSLFLLPF-FFVFTFADYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGT
QTAALSTALFNSGQKCGACFELTCEDDPEWCIPGSIIVSATNFCPPNFALANDNGGWCNP
                                                                                     YSHILFLSLCTLNFCLYSINSDDNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGL
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255
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73.6%;
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ALPHA EXPANSIN 2.
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
T -> Q (IN REF. 2).
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Pred. No. 8.1e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             family.
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3.1e-81;
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                                                                            EMBL; AC004138; AAC32927.1; -.
PIR; C84444; C84444.
InterPro; IPR007112; Expan_endogl.
InterPro; IPR007118; Expan_Lol_pl.
InterPro; IPR007117; Expan_Lol_pl.
InterPro; IPR00717; Expan_Lol_pl.
Pfam; PP01357; Pollen allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D. Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-expansin 15 precursor (At-EXP15) (AtEX15)
EXP15 OR ATZG03090 OR T17M13.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARATH
          ProDom; PD002179; Expan Lol pI C; 1.
PROSITE; PS50843; EXPANSIN CBD; 1.
PROSITE; PS50842; EXPANSIN EG45; 1.
Cell wall; Signal; Multigene family.
                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cell-wall bound.
-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
-!- SIMILARITY: Contains 1 expansin-like CBD domain.
-!- SIMILARITY: Contains 1 expansin-like CBD domain.
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MEDLINE=20083487; PubMed=10617197;
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Bukaryota; Viridiplanntae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SIGNAL
                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Causes loosening and extension of plant disrupting noncovalent bonding between cellulose matrix glucans. No enzymatic activity has been for
                                                                                                                                                                                                                                                                                                                                                  DATABASE: NAME=EXPANSIN homepage; www.bio.psu.edu/expansins/".
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RESULT RE
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P SEQUENCE FROM N.A.

C STRAINS-CV. Columbia;

C STRAINS-E20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town L., Ra, Lin X., Kaul S., Rounsley S.D., Shea T.P., Barnstead M.E., Feldblyum T.V., RA, Lin X., Ketchum K.A., Lee J.J., Romning C.M., Koo H.L., RA, Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., RA Moffat K.S., Cronin L.A., Shen M.D., Carrera A.J., Creasy T.H., RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
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                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs)
SSP consortium (Salk/Stanford/PGEC).";
SSP consortium (Salk/Stanford/PGEC).";
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O48818;
28-FEB-2003
                                                                                        Durachko D.M., Cosgrove D.J.; "Expression patterns for selective expansin genes in Arabidopsis."; (In) Abstracts of Plant Biology '99: The annual meeting of the American Society of Plant Physiologists, abstract#56, Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-expansin 4 precursor (At-EXP4) (AtEx4)
EXP4 OR AT2639700 OR F17A14.7.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryo
Spermatophyta, Magnoliophyta; eudicotyledons;
eurosids II, Brassicales, Brassicaceae, Arabio
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28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
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FUNCTION: Causes loosen disrupting noncovalent matrix glucans. No enzy similarity).
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EXPANSIN-LIKE CBD.
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C O9M259;
C O9M259;
T 28-FEB-2003 (Rel. 41, Created)
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
T 28-FEB-2003 (Rel. 41, Last sequence update)
E Alpha-expansin 16 precursor (At-EXP16) (AtEX16) (Ath-Exp. 16)
E Alpha-expansin 16 precursor (At-EXP16) (AteX16) (Ath-Exp. 17)
E Alpha-expansin 16 precursor (At-EXP16) (Ath-Exp. 17)
E Alpha-expansin 16 precursor (At-EXP16) (Ath-Exp. 17)
E Alpha-expansin 16 precursor (At-EXP16) (Ath-Exp. 17)
E Explication (Mouse-ear Cress)
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
C Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR007112; Expan_endogl.

InterPro; IPR007118; Expan_Lol_pI.

InterPro; IPR007117; Expan_Lol_pI_C.

Pfam; PF01357; Pollen_allergen; 1.

PRINTS; PR01225; EXPANSINPAMLY.

PRODOm; PD002179; Expan_Lol_pI_C; 1.

PROSITE; PS50843; EXPANSIN_EG45; 1.

PROSITE; PS50842; EXPANSIN_EG45; 1.
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1 20 POTENTIAL.
21 257 AALPHA-EXPANSIN 4.
ALPHA-EXPANSIN-LIKE EG45.
173 252 EXPANSIN-LIKE CBD.
257 AA; 27847 MW; 5C510E930A35B736 CRC64;
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RA Salanoubat M., Lencke K., Rieger M., Ansorge W., Unseld M.,
Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Ariiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Winchach B., Drzonek H., Brile H., Jordan N., Bangett S.,
RA Winchach B., Drzonek H., Erfle H., Jordan N., Bangett S.,
RA Winchach B., Wangelo M., Pallavicini A., Toppo S., Simionati B.,
RA Winchach B., Wangelo M., Pallavicini A., Toppo S., Simionati B.,
RA Winchelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D.,
RA Rooney P., Collado C., Perez-Perez A., Ottenweelder B., Masuy D.,
RA Mannhaupt G., Haase D., Serger-Llauro C., Purnelle B., Masuy D.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldbyum T.V.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldbyum T.V.,
RA Pai G., Militscher J., Selsers S.L., White O., Venter J.C.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Sasmacto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Watanabe A., Yanada M., Yasuda M., Tabata S.,
RT Takeuch A., Wada T.,
Radional Yeis of chromosome 3 of the plant Arabidopsis
Query Match
Best Local Sim
Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                           PRINTS; PR01225; EXPANSNFAMLY.

PRODOM; PD002179; EXPANI Lol pi C; 1.

PROSITE; PS50843; EXPANSIN CBD; 1.

PROSITE; PS50842; EXPANSIN EG45; 1.

Cell wall; Signal; Multigene family.
                                                                                                                                                                                                                                                                                              PIR; T47689; T47689.
InterPro; IPR007112; Expan endogl.
InterPro; IPR007117; Expan Lol pI.
InterPro; IPR007117; Expan Lol pI C.
Pfam; PF01357; Pollen allergen; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL132975; CAB75908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBCELLULAR LOCATION: Cell-wall bound.
SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 expansin-like SIMILARITY: Contains 1 expansin-like DATABASE: NAME=EXPANSIN homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Causes loosening and extension of plant cell walls l disrupting noncovalent bonding between cellulose microfibrils matrix glucans. No enzymatic activity has been found (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW="http://www.bio.psu.edu/expansins/".
                        Similarity
    Conservative
                                                                                       8
                                                                                                                                 260
260
166
                 70.2%;
67.5%;
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                                                                                         ₹
:
28;
                                                                                                         POTENTIAL.
ALPHA-EXPANSIN 16.
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
                      Score 979; DB 1;
Pred. No. 1.8e-76;
                                                                                       1428C01FCD44E994 CRC64;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EG45
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative alpha-expansin 14 precursor (At-EXP14)
ExpAlpha-1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana (Sequence features of the regions of 1,456,315 physically assigned P1 and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARATH
EX14_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98290546; PubMed=9628582; Sato S., Kaneko T., Kotani H., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expalpha-1.5).
EXP14 OR AT5G56320 OR MCD7.4.
                                                     InterPro; IPR007112; Expan_endogl.
InterPro; IPR007118; Expan_Lol_pl.
InterPro; IPR007117; Expan_Lol_pl_C.
InterPro; IPR007117; Expan_Lol_pl_C.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                          EMBL; AB009049; BAB11259.1; -
                                                                                                                                                                                                                                  or send an email to license@isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                             PRINTS; PR01225; EXPANSNFAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cell-wall bound.
SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
SIMILARITY: Contains 1 expansin-like EG45 domain.
SIMILARITY: Contains 1 expansin-like CBD domain.
DATABASE: NAME-EXPANSIN homepage;
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edons; core eudicots; Rosid
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5 bp covered
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ProDom; PD002179; Expan\_Lol\_pI\_C;

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                                                                                                                                                                                                                      STRAIN=cv. Columbia;

MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feld

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.I

Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., (

Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy

Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.

Nierman W.C., White O., Eisen J.A., Salzberg S.L., Frase
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  This SWI
between
the Euro
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Alpha-expansin 3 precursor (At-EXP3) (AtEX3)
EXP3 OR AT2G37640 OR F13M22.14.
Arabidopsis thaliana (Mouse-ear Cress).
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                "Sequence and thaliana.";
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                                                                                                                                                                        Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                080932;
                                            matrix glucans. No enzymatic activity has bee similarity).

1. SUBCELULAR LOCATION: Cell-wall bound.

1. SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

1. SIMILARITY: Contains 1 expansin-like EG45 dom:

1. SIMILARITY: Contains 1 expansin-like CBD dom:

1. DATABASE: NAME=EXPANSIN homepage;

WWW-"http://www.bio.psu.edu/expansins/".
                                                                                                                                         FUNCTION: Causes loosening and extension of plant ce disrupting noncovalent bonding between cellulose mic matrix glucans. No enzymatic activity has been found
     European
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARATH
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PS50842;
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PUTATIVE ALPHA-EXPANSIN 14.

EXPANSIN-LIKE EG45.

EXPANSIN-LIKE CBD.
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Preuss D.,
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1 28-FEB-2003 (Rel. 41, Last sequence update)

1 28-FEB-2003 (Rel. 41, Last sequence update)

1 28-FEB-2003 (Rel. 41, Last annotation update)

2 Refeb-2003 (Rel. 41, Last sequence (AtEx6) (Ath-ExpAlp

2 Representation (Rel. 41, Last sequence (AtEx6) (Ath-ExpAlp

2 Refeb-2003 (Rel. 41, Last sequence (Atex6) (Ath-ExpAlp

2 Refeb-2003 (Rel. 41, Last sequence (Atex6) (Ath-ExpAlp

2 Refeb-2003 (Rel. 41, Last sequence update)

3 Refeb-2003 (Rel. 41, Last sequence update)

4 Refeb-2003 (Rel. 41, Last sequence update)

5 Refeb-2003 (Rel. 41, Last sequence update)

5 Refeb-2003 (Rel. 41, Last sequence update)

6 Refeb-2003 (Rel. 41, Last sequence update)

7 Refeb-2003 (Rel. 41, Last sequence update)

8 Refeb-2003 (Rel. 41, Last sequence update)

9 Refeb-2003 (Rel. 41, Last sequence update)

9 Refeb-2003 (Rel. 41, Last sequence update)

9 Refeb-2003 (Rel. 41, Last sequence update)

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2 Refeb-2003 (Rel. 41, Last sequence update)

3 Refeb-2003 (Rel. 41, Last sequence update)

4 Refeb-2003 (Rel. 41, Last sequence update)

2 Refeb-2003 (Rel. 41, Last sequence update)

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R InterPro; IPR007118; Expan Lol_pi.
R InterPro; IPR007118; Expan Lol_pi.
C InterPro; IPR007117; Expan Lol_pi.C.
Pfam; pP01357; Pollen allergen; 1.
PRINTS; PR01225; EXPANSNPAMLY.
PRODom; PD002179; Expan Lol_pi.C.; 1.
PROSITE; PS00843; EXPANSIN E045; 1.
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SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLINE=20083487; PubMed=10617197
Lin X., Kaul S., Rounsley S.D., S
Fujii C.Y., Mason T.M., Bowman C.
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
MEDLINE=96016146; PubMed=7568110;
MEDLINE=96016146; PubMed=7568110;
Shcherban T.Y., Shi J., Durachko D.M., Guiltinan
McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
"Molecular cloning and sequence analysis of expar
conserved, multigene family of proteins that medi
extension in plants.";
Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
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                        PubMed=10617197;
Rounsley S.D., Sh
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EXPANSIN-LIKE CBD.
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T.P., Benito M.-I., Town (Barnstead M.E., Feldblyum
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Matches 161
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InterPro; IPR007118; Expan_Lol_pi.
InterPro; IPR007118; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi.
Pfam; Pf01357; Pollen_allergen; 1.
PR1NTS; PR01225; EXPANUSIRAMLY.
PRODOm; PD002179; Expan_Lol_pi.C; 1.
PROSITE; PS50843; EXPANSIN_EGB; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
PARATH
EXP9 ARATH
Q9LZ99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moffat K.S., Ketchum K.A., Lee J.J., Ronning C.M., Koo I Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creas Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss Nierman W.C., White O., Eisen J.A., Salzharra C., Venter T.C.
                                                                                                                                                                                                                                                                                   CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U30480; AAB38072.1; -.
EMBL; AC005315; AAC33223.1; -.
PIR; T02727; T02727.
PIR; T50653; T50653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thaliana."
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                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matrix glucans. No enzymatic activity has been fo similarity).

SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

SIMILARITY: Contains 1 expansin-like EG45 domain.

SIMILARITY: Contains 1 expansin-like CBD domain.

SIMILARITY: Contains 1 expansin-like CBD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WWW="http://www.bio.psu.edu/expansins/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Causes loosening and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disrupting noncovalent bonding
                                                                                     204
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                                                                                                                                                                                                GGWETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGFSCGACFELKC
                                                                                                                                                                                                             GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
                                                                                                           VPVSFRRVPCKKRGGIRFTINGFRYFNLVLVINVAGAGNIVRLGVKGTHTSWMTMSRNWG
                                                                                                                      VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                                                                                                      ASDPKWCHSGSPSIFITATNFCPPNFAQPSDNGGWCNPPRPHFDLAMPMFLKIAEYRAGI
                                                                 QNWQSNSVLVGQSLSFRVTSSDRRSSTSWNIAPANWKFGQTFMGKNF
                                                                              ONWOSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
                                                                                                                                                                     TNDPKWCLPG--TIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMABPAFLQIAQYRAGI
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175
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            STANDARD;
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                                                                                                                                                                                                                                                                                     28004 MW;
                                                                                                                                                                                                                                                    67.48;
                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                              EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
MISSING (IN REF. 2)
                                                                                                                                                                                                                                                    Score 939; DB 1;
Pred. No. 4.7e-73;
                                                                                                                                                                                                                                                                                                                            family.
POTENTIAL.
ALPHA-EXPANSIN 6.
           PRT;
                                                                                                                                                                                                                                                                                   B0C8089F0222C908 CRC64;
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extension of plant cell walls by between cellulose microfibrils as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 of the plant Arabidopsis
           258 AA
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                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aken S., Umayam
J., Creasy T.H.,
                                                                                                                                                                                                                                                             Length 259;
                                                                                                                                                                                                                                        Indels
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RX MEDLINE-21016721; Pubmed-11130714;
RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Agamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Mutsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., de la Bastide M.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., de la Bastide M.,
RA Natinabe A., Yamada M., Sato S., de la Bastide M.,
RA Stoneking T., Pepin K., Spieth J., Schhon M., Armstrong J., Becker M.,
RA Stoneking T., Pepin K., Spieth J., Schhon M., Armstrong J., Becker M.,
RA Habermann K., Cordum H., Cordes M., Courtney W., Dante M.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., MacCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Ransperger U., Wedler H., Balke K., Wedler E., Johnson S.,
RA Ransperger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Weltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Weltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Weltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.;
"For Italian T., Thomas M., Marian M., Pransz P.;
"Sequence and analysis of chromosome 5 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. Columbia;

STRAIN-CV. Columbia;

STRAIN-CV. Columbia;

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Causes loosening and extension of plant cell walls be disrupting noncovalent bonding between cellulose microfibrils disrupting noncovalent bonding between cellulose microfibrils

of the Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-expansin 9 precursor (At-EXP9) (AtEx9) (Ath-ExpAlpha-1.10).
EXP9 OR AT5G02260 OR T1E22_20.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                              PIR;
                                                                                                                                                                              EMBL; AL162874; CAB85531.1;
EMBL; AY054586; AAK96777.1;
                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBCELLULAR LOCATION: Cell-wall bound.
SUBCELLULAR LOCATION: Cell-wall bound.
SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
SIMILARITY: Contains 1 expansin-like CBD do
SIMILARITY: Contains 1 expansin-like CBD do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WWW="http://www.bio.psu.edu/expansins/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATABASE: NAME=EXPANSIN homepage;
                                                                                                                                              T48247; T48247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408:823-826(2000).
             IPR007112;
IPR007118;
IPR007117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Columbia;
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; Expan_endogl.
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; Expan_Lol_pI_(
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MBL outstation -
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RESULT 12
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PRINT'S; PR01225; EXPANISHPAMLY.
PRODOM; PD002179; Expan_Lol_pl_C; 1
PROSITE; PS50843; EXPANSIN_EG45; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
Cell wall; Signal; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-96016146; PubMed=7568110;

MEDLINE-96016146; PubMed=7568110;

Shicherban T.Y., Shi J., Durachko D.M., Guiltinan McQueen-Mason S.J., Shieh M., Cosgrove D.J.;

"Molecular cloning and sequence analysis of expan "Molecular cloning and sequence analysis of expan conserved, multigene family of proteins that medi extension in plants.";

Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Alpha-expansin 5 precursor (At-EXP5) (AtEx5) (Ath-ExpAlpha-1.4).
Alpha-expansin 5 precursor (At-EXP5) (AtEx5) (Ath-ExpAlpha-1.4).
EXP5 OR AT3G29030 OR K5K13_14 OR K5K13.16.
Arabidopsis thaliana (Mouse-ear cress) Embryophyta; Tracheophyt Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyt Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Roseurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q38864;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
MEDLINE=20277480; PubMed=10819329;
Sato S., Nakamura Y., Kaneko T., Katoh T.,
"Structural analysis of Arabidopsis thaliar
features of the regions of 4,504,864 bp cov
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SEQUENCE
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Res. 7:131-135(2000).

FUNCTION: Causes loosening and extension of plant cell walls be disrupting noncovalent bonding between cellulose microfibrils matrix glucans. No enzymatic activity has been found (By similarity).

SUBCELLULAR LOCATION: Cell-wall bound.

SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

SIMILARITY: Contains 1 expansin-like EG45 domain.

SIMILARITY: Contains 1 expansin-like CBD domain.
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thaliana chromosome 3
4 bp covered by sixty
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Best Local S
Matches 157
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Q9LNU3;
28-FEB-2003
28-FEB-2003
28-FEB-2003
SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Ka White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin Buehler E., Chan L., Conway A.B., Conway A.R., Creasy T. Chung M.K., Conn L., Conway A.B., Conway A.R., Fong B., F
                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-expansin 11 precursor (At-EXP11) (AtEx11) (Ath-EXP11 OR ATIG20190 OR T20H2.4 OR T20H2_5.

EXP11 OR ATIG20190 OR T20H2.4 OR T20H2_5.

Experimentation of the sequence of the sequen
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PROSITE; PS50843; EXPANSIN CBD; 1.
PROSITE; PS50842; EXPANSIN.EG45; 1.
Cell wall; Signal; Multigene family.
Cell wall; Mul
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Expan_endogl.

InterPro; IPR007111; Expan_Lol_pi.

InterPro; IPR007117; Expan_Lol_pi C.

Pfam; PF01357; Pollen_allergen; 1.

PRINTS; PR01225; EXPANSNEAMLY.
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EMBL; AB025615; BAA95756.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMB European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content in the content of the content is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATABASE: NAME=EXPANSIN homepage; WWW="http://www.bio.psu.edu/expansins/".
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Pred. No. 7.
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
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Fujii C
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                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                    EMBL; AC022472; AAF79895.1; -. EMBL; AF332436; AAG48799.1; -. PIR; F86335; F86335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length colones (RAFLs) sequenced SSP consortium (Salk/Stanford/PGEC)."; submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Expression patterns for selective expansin genes in F
(In) Abstracts of Plant Biology '99: The annual meetir
American Society of Plant Physiologists, abstract#56,
                                                                                                                                                                                                                  ProDom; PD002179; Expan Lol pI C; 1.
PROSITE; PS50843; EXPANSIN CBD; 1.
PROSITE; PS50842; EXPANSIN EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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InterPro; IPR007118; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi_C.
Pfam; PF01357; Pollen_allergen; 1.
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                                                                                                                                                                                                                                                                      PRINTS; PR01225; EXPAÑSNFAMLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epidermis or in the vascular bundles.
SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
SIMILARITY: Contains 1 expansin-like EG45 d
SIMILARITY: Contains 1 expansin-like CBD do
DATABASE: NAME=EXPANSIN homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBCELLULAR LOCATION: Cell-wall bound.
TISSUE SPECIFICITY: Expressed in the 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Causes loosening and extension of plant cell walls by disrupting noncovalent bonding between cellulose microfibrils amatrix glucans. No enzymatic activity has been found (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWW="http://www.bio.psu.edu/expansins/".
                                                     155;
27 GWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTCT
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                                                                   Similarity
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44
169
252
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159
                                                                 62.1%;
69.8%;
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                                                                                                                  ALPHA-EXPANSIN 11.
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
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                                                     Mismatches
                                                   e 865.5; DB 1;
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ismatches 41;
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99: The annual meeting of the
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RESULT 14
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RA Kreis M., Delseny M., Ge Simone V., Obermaler B., Mache K., Muleirer R., Ra Ra Kreis M., Delseny M., Digdomenech P., Watson M., Schmidtheini T., Ra Ra Chert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Ra Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Ra Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Ra Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Ra Langham S.-A., Edition J., Voet M., Bastiaens I., Aert R., Defoor E., Ra Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ra Holzer S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Ra Berneiser S., Hempel S., Feldpausch M., Lamberth S., van den Daele H., Ra Clark L., Doggett J., Hall S., Kay M., Lamnard N., McLay K., Mayes R., Ra Clark L., Doggett J., Hall S., Kay M., Lannard N., McLay K., Mayes R., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Ra Clark L., Doggett J., Vitale D., Liguori R., Piravandi E., Ra Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller Auer S., Gabel C., Puthe M., Fartmann B., Granderath K., Dauner D., Herzl A., Ra Gabel C., Puthe M., Fartmann B., Granderath K., Dauner D., Herzl A., Ra Gabel C., Puthe M., Fartmann B., Granderath K., Dauner D., Jesse T., Ra Gabel C., Puthe M., Perper C., Monfort A., Casacuberta B., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Ra Gibbons T., Weber N., Waller N., Getot S., Tacon D., Jesse T., Ra Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Ra Pattella P., Bevan M., Ghoj L., Schutz K., Hang B., Lageld L., Ra Kamer J., Fulton L., Marcis B., Miller N., Greo T., Kemp K., Ra Kamer J., Pether K., Cotton M., Joshu C., Layman D., Ra Antonoi
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28-FEB-2003
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MEDLINE=20083488; PubMed=10617198;
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EXP17 OR AT4G01630 OR T15B16.16.
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(Rel. 41, Last annotation update)
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InterPro; IPR007117; Expan_Lol_pI.
Pfam; PP01357; Pollen allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Expan_Lol_pI_C; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no may modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix glucans. No enzymatic activity has b similarity).
Similarity: Cell-wall bound.
SIMCLARITY: BELONGS TO THE EXPANSIN FAMILY.
SIMILARITY: Contains 1 expansin-like EG45 do SIMILARITY: Contains 1 expansin-like EDB do DATABASE: NAME-EXPANSIN homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Causes loosening and extension of plant cell walls disrupting noncovalent bonding between cellulose microfibrile matrix glucans. No enzymatic activity has been found (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWW="http://www.bio.psu.edu/expansins/"
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152; Conserv
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46
171
255 AA;
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                STANDARD;
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Pred. No. 1.76
87; Mismatches
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PUTATIVE ALPHA-EXPANSIN
EXPANSIN-LIKE EG45.

EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A33A62D3522A530F
                273
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ches 50;
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R InterPro; IPR0071112; Expan_nendogi.

R InterPro; IPR0071112; Expan_Lol_pi.

R InterPro; IPR0071113; Expan_Lol_pi.

R InterPro; IPR007111; Expan_Lol_pi.

R Pfam; PF01357; Pollen allergen; 1.

R Pfam; PF01275; Expan_Lol_pi.C; 1.

R PROSITE; PS001275; Expan_Lol_pi.C; 1.

R PROSITE; PS50843; EXPANSIN_CBD; 1.

R PROSITE; PS50842; EXPANSIN_CBD; 1.

R PROSITE; PS50842; EXPANSIN_EMBL; Signal; Multigene famil FOLDAIN

T SIGNAL

1 21 273 PUTATIVE ALPHA-EXPANSIN 22.

T DOMAIN 190 269 EXPANSIN-LIKE EG45.

T DOMAIN 190 269 EXPANSIN-LIKE CBD.
                                                                                                                                      Query Match
Best Local :
                                                                                                                         Matches
                                                                                                                                                                                     DOMAIN
DOMAIN
SEQUENCE
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Unpublished ob
-!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=98344145; PubMed=9679202;
Kaneko T., Kotani H., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative alpha-expansin 22 precursor (At-EXP22) (AtEx22) (AtExpAlpha-1.15).

EXPALPHA-1.15).

EXPALPHA-1.15).

EXPALPHA-1.15).

EXPALPHA-1.15).

EXPALPHA-1.15).

EXPALPHA-1.16).

EXPALPHA-1.16).

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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28-FEB-2003
28-FEB-2003
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DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                         or send
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SUBCELLULAR LOCATION: Cell-wall bound.

SUBCELLULAR LOCATION: Cell-wall bound.

SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

SIMILARITY: Contains 1 expansin-like EG45 domain.

SIMILARITY: Contains 1 expansin-like CBD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene model prediction.
DATABASE: NAME=EXPANSIN homepage;
WWW="http://www.bio.psu.edu/expansins/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iblished observations (DEC-2001). FUNCTION: Causes loosening and extension of plant cell walls disrupting noncovalent bonding between cellulose microfibrils matrix glucans. No enzymatic activity has been found (By
109
                           85
                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                       Similarity
              CTNDPKWCLPGTIRVTATNPCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIV
                                                         WQSGHATFYG---GGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMT
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CTRDPQWCLPGSVKITATNFCPANYS -- KTTDLWCNPPQKHFDLSLAMFLKIAKYKAGVV
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Pred. No. 9.
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Search o Job time	ф	δ	Дb	δ
Search completed: December 18, 2003, 17:48:59 Job time : 19 secs	227 NWTTITVLTGQGLSERVTTSDGITKDEWNVMPKNWGFGQTFDG 269	205 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEG 247	167 PVRYRRIPCSKTGGVKFETKGNPYFLMVLIYNVGGAGDIKYVQVKGNKTGWITMKKNWGQ 226	145 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 204

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1394
1 MAFSYSPFSSLFLLPFFFVF.....AYNLVPSNWQFGQTYEGPQF 250
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                           sp_invertebrate:*
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sp_virus:*
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match I	Length	80 1	ID	Description
1	1394	100.0	250	10	Q39625	Q39625 cucumis sat
2	1160.5	83.2	254	10	082093	
ω	1152.5	82.7	260	10	Q9FNT0	_
4	1151.5	82.6	254	10	Q9FUM3	
5	1143.5	82.0	245	10	Q9LLB2	
6	1130.5	81.1	253	10	Q8L5S7	
7	1125	80.7	247	10	082625	
8	1118	80.2	249	10	Q9ZP35	Ŀ
9	1117.5	80.2	253	10	Q9SBT1	
10	1116.5	80.1	253	10	Q9SWD4	
11	1116	80.1	254	10	Q8RVK6	
12	1113.5	79.9	253	10	Q93XP2	
13	1111	79.7	252	10	Q9FS30	Q9fs30 prunus pers
14	1108	79.5	252	10	Q8L5S6	
15	1105	79.3	252	10	081133	
16	1102.5	79.1	255	10	Q8RVK4	

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1002	1008.5	1022	1024	1027	1027	1027	1029	1030	1030	1032	1037	1038	1039	1041	1041.5	1043	1048	1050	1051	1053	1058	1059	1063	1077	1085	1087	1092	1101.5
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Q9fvg9 lycopersico	zinnia ele		arabidops	Q94kt7 zea mays (m	Q9m5i5 triphysaria	Q81kj8 gossypium h	Q815r7 rumex palus	Q815g1 rumex palus	rumex		prunus av	oryza	Q946j0 oryza sativ	Q8let9 arabidopsis	Q9m5i7 triphysaria	Q40636 oryza gativ	cicer a	prunue				доввур	Q815g5 cicer ariet	pinus	pinus	2 pinus	3 pinus	Q9swyl pinus taeda

## ALIGNMENTS

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Query Match 100.0%; Score 1394; DB 10; L Best Local Similarity 100.0%; Pred. No. 7.1e-118;	SQ SEQUENCE 250 AA; 27215 MW; 60651BC47E4186DA CRC64	PROSTIE; PS50842; EXPANSIN_EG45; 1.	PROSITE;	ProDom; PD002179;	PRINTS; PR01225; EXPANSNFAMLY.	Pfam; PF01357; Pollen allergen; 1.	InterPro; IPR007117; Expan Lo	DR InterPro; IPR007118; Expan Lol pI.		EMBL; U30382; AAB37746.1;		RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).	extension :	conserved, multigene family of proteins that	"Molecular cloning and sequence analys	RA McOueen-Mason S.J., Shieh M., Cosgrove D.J.;	Chebarhan H V Chi I Diversión D M		SEQUENCE PROM				Spermatophyta; Magnoliophyta; eudicotyledons; core	Eukaryota; Virio	Cucumis		Expansin S1.	01-MAR-2003 (TrEMBLrel. 23, Last annotation	01-NOV-1996 (TrEMBLrel. 01,		039625.	ID 039625 PRELIMINARY; PRT; 250 AA.	RESULT 1	
Length 250;	**				•									cell wall		•			٠				eudicots; Rosidae;	Tracheophyta;										

Rosidae;

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Best Local S
Matches 206
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Mbeguie A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;

Mbeguie A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;

Molecular cloning and nucleotide sequence of expansin 1 (I

from apricot fruit ";

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

EMBL; U93167; AAC33529.1; -.

REMBL; U93167; AAC33529.1; -.

REMBL; U93167; AAC33529.1; -.

RINTERPRO; IPR007112; Expan_Lol_pi.

InterPro; IPR007118; Expan_Lol_pi.

RINTERPO; IPR007117; Expan_Lol_pi.

PRINTS; PR0125; EXPANSIN_EGAF; 1.

PRLNTS; PR01279; Expan_Lol_pi.

REPODOM; PD002179; Expan_Lol_pi.

REPODOM; PD002179; Expan_Lol_pi.

REPODOM; PD002179; EXPANSIN_EGAF; 1.

RESOIRE PS50842; EXPANSIN_EGAF; 1.

RESOIRE PS50842; EXPANSIN_EGAF; 1.
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082093;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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GDVHSVSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQ
                                                        PPLQHEDMAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGA
                                                                                                              TNTAALSTALFNNGLSCGSCYEMRCNNDPRWCRPGSIIVTATNFCPPNFAQSNDNGGWCN
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Last annotation update)
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Pred. No. 8.6e
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Best Local S
Matches 203
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"An second expansin is expressed in chickpea epicotyls.";

Submitted (DEC-2000) to the EMBL/GenBank/DDJ databases.

-:- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.

REMBL; AJ291817; CAC19184.1;

RINTEPTO; IPR007112; Expan endogl.

RINTEPTO; IPR007117; Expan Endlyl.

RINTEPTO; IPR007117; Expan Lol DI.

RINTEPTO; IPR000504; RNA rec_mot.

RINTEPTO; IPR000504; RNA rec_mot.

RINTEPTO; IPR000504; RNA rec_mot.

RPINTS; PR01225; EXPANSINFAMLY.

RPROSITE; PS01225; EXPANSIN ESG45; 1.

PROSITE; PS00843; EXPANSIN ESG45; 1.

PROSITE; PS00030; RRM RNP T; 1.

PROSITE; PS00031; RRM RNP T; 1.

PROSITE; PS00031; RRM RNP T; 1.
Q9FUM3;
Q9FUM3;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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STRAIN=cv. Castellana;
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Best Local Sim
Matches 205;
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C SPECIES-P. GAO Z., Cantini C., Loescher W., van Nocker S.;
Voo S.-D., GAO Z., Cantini C., Loescher W., van Nocker S.;
Voo S.-D., GAO Z., Cantini C., Loescher W., van Nocker S.;
Van Coordinated expression of genes encoding expansins and other cell
VT wall-modifying enzymes is associated with pectin-related changes in
VT the cell wall during ripening of cherry (P. cerasus) fruit.";
VI Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
VC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
VC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
VR EMBL; AF350937; AAK48046.1; -.
VR EMBL; AF350937; AAK48046.1; -.
VR InterPro; IPR007112; EXPAN Endogl.
VR InterPro; IPR007118; EXPAN_LOl_DI.
VR InterPro; IPR007118; EXPAN_LOl_DI.
VR InterPro; IPR007118; EXPAN_LOl_DI.
VR PRINTS; PR01275; EXPAN_SIN_FAMILY.
VR PRINTS; PR01275; EXPAN_SIN_FAMILY.
VR PROSITE; PS500412; EXPANSIN_EG45; 1.
VR PROSITE; PS500412; EXPANSIN_EG45; 1.
VR PROSITE; PS500412; EXPANSIN_EG45; 1.
                                                                                                                                    Q9LLB2;
01-OCT-2000
01-OCT-2000
01-MAR-2003
Expansin 2.
   Spermatophyta; Magnolio; Asteridae; campanulids;
                                                                     Zinnia elegans.
Eukaryota; Viridiplantae;
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"Differential Expression
(Prunus avium L.) During
Submitted (AUG-2000) to t
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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EXP1 OR EXP2.
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liophyta; eudicotyledons; core eudicots;
ls; Asterales; Asteraceae; Asteroideae;
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g Fruit Ripening.";
the EMBL/GenBank/DDBJ
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Pred. No. 5.6e-96;
4; Mismatches 30
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on update)
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RESULT
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"The expression of expansin genes : Rumex palustris.";
Submitted (OCT-2001) to the EMBL/Ge -: SIMILARITY: BELONGS TO THE EXPA EMBL; AF428174; AAM22621.1; -- InterPro; IPR007112; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi.
CPfam; PF01357; Pollen allergen. 1
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Best Local Similarity
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"Subcellular localization of expansin mRNA in xyler
Plant physiol. 123:463-470(2000).
-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
EMBL; AF230332; AAF35901.1;
-InterPro; IPR007112; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi.
C. Pfam; PF01357; Pollen allergen; 1.
PRINTS; PR01225; EXPANSINFAMLY.
PRODOM; PD0102179; Expan_Lol_pi_C: 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
SEQUENCE 245 AA; 26201 MW; F66E26114C27E380 CR0
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Q8L5S7;
01-OCT-2002
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01-MAR-2003
Expansin 7 p
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eucaryophyllidae; Caryophyllales; Polygonaceae; Rumex.
                                                                                                                                                                                      Peeters A.J.M.;
                                                                                                                                                                                                                                     Colmer T., Wagemaker
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=50298;
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TISSUE=Root/shoot
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MEDLINE=20317189;
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NCBI_TaxID=34245;
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ker C.A.M.,
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Pred. No. 2.8e-95;
Pred. No. 2.8e-95;
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                                                                                                                       EXPANSIN
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Best Local S
Matches 205
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998
01-NOV-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                     082625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01225; EXPANSNFAMLY.

ProDom; PD002179; Expan Lol pi C; 1

PROSITE; PS50843; EXPANSIN CBD; 1.

PROSITE; PS50842; EXPANSIN EG45; 1.

Signal.

25 POTENT

SIGNAL 1 25 POTENT
                                                                                                                                                                                                                       expansin.";
Submitted (
                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Solanum.
PRINTS; PRO1225; EXPAÑSNFAMÍY.

PRODOM; PD002179; EXPAN LOL DI C; 1.

PROSITE; PS50843; EXPANSIN EG45; 1.

PROSITE; PS50842; EXPANSIN EG45; 1.
                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. VFN8;
Caderas D., Muster M., Vogler H., Mandel T., Rose J.,
McQueen-Mason S., Kuhlemeler C.;
"Limited correlation between expansin gene expression
                                                                                                                                                                                                                                         TISSUE=Hypocotyl;
Catala C., Rose J.K.C.,
"Hormonal regulation an
                                                                                                                                                                                                                                                                                                                                                                          EXPANSIN.
                                           InterPro; IPR007112; Expan endogl.
InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI_C.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                         growth rate.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                               EEXP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WCNPPLQHFDMAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYGTNTVALSTALFUNGLSCGACFEMTCTINDFKWCLPGTIRVTATNFCPPNFALPNNNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAFSYSPFSSLFLLPF--FFVFTFADYGG-WQSGHATFYGGGDASGTMGGACGYGNLYSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGDVH5V8IKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WCNPPLQHFDLAEPAFLQIAQYHAGIVPVSFRRVPCGRKGGIRFTVNGHSYFNLVLITNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYGTSTAALSTALFNNGLSCGACFEMKCTADPRWCIGGVITVTATNFCPPNFALANDNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWQFGQTFEGSQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NWOFGOTYEGPOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGDVHSVSIKGSSGGWQAMSRNWGQNWQSNSYLNGQSLSFMVTTSDGRTLTSSNVAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAFQAFLASSLLLIAFQHFVSSAFGDYGGDWNGGHATFYGGGDASGTMGGACGYGNLYSQ
                                                                                                                                                                                                                        (OCT-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
26765 MW;
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                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%; Score 1130.5; DB
81.0%; Pred. No. 4.4e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                         Bennett
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                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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; SAD64CA8563306C7 CRC64;
                                                                                                                                                                                                                                                         A.B.,
                                                                                                                                                                                                                                             patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                    247
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                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                             of LeEXP2,
                                                                                                                              databases
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                                                                                                                                                                                                                                               new
                                                                                                                                                     elongation
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RESULT
Q9ZP35
ID Q9
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                                                                                     Query Match
Best Local S
Matches 201
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ZP35;
Q9ZP35;
01-MAY-1999
01-MAY-1999
01-MAR-2003
                                                                                                                                Signal.
NON TER
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                "Acid-growth response and alpha-expansins in suspension cultures bright yellow 2 tobacco.";
Plant Physiol. 118:907-916(1998).
-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
EMBL; AF049354; AAC96081.1;
-InterPro; IPR007112; Expan_endogl.
InterPro; IPR007112; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnaliophyta; eudicotyledons; core eu
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                      PRINTS; PR01225; EXPANSNEAMLY.
PROBLITE; PS50843; EXPANSIN CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99026292; PubMed=9808735;
                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-expansin
                                                                                                                                                                                                                                                                                                                                    ink B.M.,
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                                                                                       201;
63
                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                 Similarity
           VALSTALFNNGLSCGACFEMTCTNDPKWCLPGTIRVTATNPCPPNFALPNNNGGWCNPPL
                                        NTGWQAMSRNWGQNWQSNSNLNGQSLSFQVTTSDGRTLISNNAAPNNWQFGQTFBGAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISFCFYSTFADYGGWQTAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLLPFFFVFTFADYGGWOSGHATFYGGGDASGTWGGACGYGNLYSOGYGTNTVALSTALF
AALSTALFUNGLTCGACYELTCUNDGQSCLQGSIIVTATNFCPPNPSLPNNNGGWCNPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNGLTCGACYELTCNNAAQWCLQGTITVTATNFCPPNPSLPNNNGGWCNPPLQHFDLAQP
                                                                                                                            1
<1
23
249
                                                                                                                                                                                                                                                                                                                                      Cosgrove
                                                                                                                                                                                                                                                                                                                                                            BY2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 AA;
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBirel. 10, Created)
(TrEMBirel. 10, Last sequence update)
(TrEMBirel. 23, Last annotation updat
sin precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                  A,
                                                                                                                      1
22
249
26663 F
                                                                                                                                                                                                                                                                                                                                      D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.7%;
                                                                                                80.2%;
                                                                                                                                  WW;
                                                                                       19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1125; DI
Pred. No. 1.3e
21; Mismatches
                                                                                      Score 1118; DB 10
Pred. No. 5.8e-93;
9; Mismatches 23
                                                                                                                                 POTENTIAL.
ALPHA-EXPANSIN.
9B223A43CA952879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99E6F53F84F7A3E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
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                                                                                                            10;
                                                                                      23;
                                                                                                                                  CRC64;
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                                                                                        Indels
                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                     eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                              Tracheophyta;
                                                                                                              249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247;
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 122
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RESULT 10
Q9SWD4
ID Q9SWD4
AC Q9SWD4;
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Best Local S
Matches 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 independent.";

plant physiol. 12:1273-1279(1999).

-!- SIMILARITY: BELONGS TO THE EXPANSIN

EMBL; AFF159563; AAFF21101.1; -.

InterPro; IPR007112; Expan_endogl.

InterPro; IPR007118; Expan_Lol_pi.

InterPro; IPR007117; Expan_Lol_pi.

InterPro; IPR007017; Expan_Lol_pi.

InterPro; IPR007018; Reg_chr_condens.

pfam; pF01357; Pollen_allergen; 1.

PRINTS; PR01225; EXPANSINEMALY.

ProDom; PD002179; Expan_Lol_pi_C; 1.

PROSITE; PS50843; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Charcivello P.M.,
"An expansin g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9SBT1;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expansin. EXP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragaria ananassa (Strawberry).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SBT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197;
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                                                                                                                                                                     RNMGQNMQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGFQF
                                                                                                                                                                                                                                                                     RAGIVÞVSFRRVÞCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMS
                                                                                                                                                                                                                                                                                                                                  CYEMRCUNDPRWCLPGSIIVTATNFCPPNFAQANDNGGWCNPPLQHFDLAEPAFLQIAQY
                                                                                                                                                                                                                                                                                                                                                             CFEMTCTNDFKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEDAFLQIAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                TYADYGAGWVGGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGS
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Chandler;
M., Sabehat A., Powell A.L.T.,
in gene expressed in ripening
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85.3%;
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Pred. No. 6.5e
                                PRT;
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Best Local Sin
Matches 201;
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Q8RVK6;
01-JUN-2002
01-JUN-2002
01-MAR-2003
Expansin 1.
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                                                                                        eurosids I; Rosa
NCBI_TaxID=3750;
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101-MAY-2000 (TrEMBLrel. 13, Created)
101-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAY-2003 (TrEMBLrel. 13, Last sequence update)
101-MAY-2
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Planta 210:956-963(2000).

Planta 210:956-963(2000).

Planta 210:956-963(2000).

Planta 210:956-963(2000).

EMBL; AF167360; ADA9956.1; -

InterPro; IPR007112; Expan endog1.

InterPro; IPR007117; Expan Lol_pi_C.

Pfam; PF0157; Pollen allergen; 1.

PRINTS; PR01225; EXPANSINAMLY.

PRODOM; PD012179; Expan Lol_pi_C.

PROSITE; PS50843; EXPANSIN_E045; 1.

PROSITE; PS50842; EXPANSIN_E045; 1.

SEQUENCE 253 AA; 27063 MW; 7DC7561.
SEQUENCE FROM N.A. STRAIN=cv. Granny Smith; Trivedi P.K., Solomos T.
                                                                                                                                                                            Malus domestica (Apple) (Malus sylvestris).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Lear; PubMed=10872228; WEDLINE=20330988; PubMed=10872228; Vriezen W.H., De Graaf B., Mariani C., Voesenek L. "Submergence induces expansin gene expression in 1 "Submergence induces expansin gene expression in 1 Rumex palustris and not in flooding-intolerant R.
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79.4%; Pred. No. 8e-
tive 16; Mismatches
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in flooding-
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RESULT 12
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ID Q93XP
AC Q93XP
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DT 01-ME
DT 01-ME
DT 01-ME
DT 01-ME
OC EXPAI
GN Prun
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OC GUCC
OX NCBJ
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RP SEQI
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Best Local S
Matches 198
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InterPro; IPR007117; Expan Lol pI C.
InterPro; IPR007117; Expan Lol pI C.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF01357; Pollen allergen; 1.
ProDom; PD002179; Expan Lol pI C; 1.
PROSITE; PS50843; EXPANSIN CBD; 1.
PROSITE; PS50842; EXPANSIN EG45; 1.
PROSITE; PS00626; RCC1 2; 1.
SEQUENCE 254 AA; 27246 MW; 23FBED3E
                InterPro; IPR007112; Expan_endog1.
InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
Pfam; PF01357; Pollen_allergen; 1.
PRXMTS; PR01225; EXPANSNPAMLY.
PRODOm; PD002179; Expan_Lol_pI_C; 1.
PROSITE; PS50843; EXPANSIN_EB45; 1.
PROSITE; PS50842; EXPANSIN_EB45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q93XP2;
Q93XP2;
01-DEC-2001
01-DEC-2001
                                                                                                                                                        YOO S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
"Coordinated expression of genes encoding expansins and other cell
wall-modifying enzymes is associated with pectin-related changes in
the cell wall during ripening of cherry (P. cerasus) fruit.";
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
-!-SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
EMBL; AF350936; AAK48845.1; -
                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

NCBI_TaxID=140311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of expansin cDNA from apple.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ da
-i-SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
EMBL; AY083166; AAM08928.1;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Fruit;
                                                                                                                                                                                                                                                                                                                                                                                                    Prunus cerasus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254
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Last sequence update)
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Pred. No. 9
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     9C24484F14AA52CD
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Best Local Similarity
Matches 201; Conserv
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InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSINFAMLY.
PRODOm; PD002179; Expan_Lol_pI_C; 1.
PROSITE; PS50843; EXPANSIN_E045; 1.
PROSITE; PS50842; EXPANSIN_E045; 1.
SEQUENCE 252 AA; 26743 MW; BF0B86F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FS30;
Q9FS30;
01-MAR-2001
01-MAR-2001
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"Homolog to expansin in peach
Submitted (JUN-1999) to the EM
-!- SIMILARITY: BELONGS TO THE
EMBL; AB029083; BAB19676.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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                                                                                                                                                                                                                                                                      MAF-SYSPESSLF-LLPFFFFVFTFADY-GGWQSGHATFYGGGDASGTWGGACGYGNLYSQ
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GGAGDVHSVSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPS
                                          WCNPPLQHFDLAEPAFLQIAQYRAGIVPVSFRRVSCVKKGGIRFTINGHSYFNLVLITNV
                                                                       WCNPPLOHFDMAEPAFLOIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNV
                                                                                                                                          GYGTNTAALSTALFNDGLSCGSCYEMRCDSDPKWCLPGSIIVTATNFCPPNLAQSNDNGG
                                                                                                                                                                                                                                    MAFTSHLAIALLFSVLNLCLQGTYGDYGGGWEGGHATFYGGGDASGTMGGACGYGNLYSQ
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EMBL/GenBank/DDBJ
THE EXPANSIN FAMIL
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Last sequence update)
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Pred. No. 2.5e-92;
1; Mismatches 25
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Pred. No. 1.5
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Best Local S
Matches 203
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InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
Pflam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSINFAMLY.
PRODOm; PD002179; Expan_Lol_pI_C; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
081133
081133;
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SIGNAL
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Rumex palustris.";
Submitted (OCT-2001) to the EMBL/GenBan)
-!- SIMILARITY: BELONGS TO THE EXPANSIN
EMBL; AF428175; AAM22622.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Root/shoot junction;
Colmer T., Wagemaker C.A.M.,
Peeters A.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Polygonaceae; Rumex. NCBI_TaxID=50298;
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-OCT-2002
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Pred. No. 4.7e
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Mbeguie-A-Mbeguie D., Fils-Lycaon B.;
"Molecular cloning and nucleotide seque
from apricot fruit.";
Submitted (DEC-1997) to the EMBL/GenBar
-!-SIMILARITY: BELONGS TO THE EXPANSI
EMBL; APO3815; AAC33530.1; -
InterPro; IPR007112; Expan_endogl.
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InterPro; IPR007117; Expan_lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
PROSTOR; PR01225; EXPANSINFAMLY.
PROSTOR; PS0125; EXPANSIN EDG; 1.
PROSTOR; PS50842; EXPANSIN_EG45; 1.
SEQUENCE 252 AA; 26758 MW; 5881AE50
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
NCBI_TaxID=36596;
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EXP2.
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Midmatches 25;
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Maximum Match 100%
Listing first 45 summaries
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-MODEL=frame+_p2n.model
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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

Query

## ALIGNMENTS

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	CD574577	RESULT 1
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Poncirus.	Poncirus trifoliata	Poncirus trifoliata	EST.	CD574577.1 GI:31670479	CD574577	UCR Poncirus trifoliata cDNA clone UCRPT01_06_G11, mRNA sequence.	UCRPT01_06_G11_T3 Poncirus trifoliata CTV-challenged cDNA library -	CD574577 880 bp mRNA linear EST 12-JUN-2003		

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                                                                                         1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePhePheValPhe
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Tel: 9097874137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Mikeal Roose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 880)
ROOSe, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D. Wanamaker, S., Choi, Y. and Kingan, T.
Development of EST Resources and New Genetic Markers for Citrus - Poncirus trifoliata CTV-challenged phloem - UCR
primer: T3
                                                                                                                                                                                                                                                                                                                                   231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anote "Wector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI, Site 2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the ML Roose lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the University of California Riverside Genomics Institute, Core Instrumentation Facility (Choi. Kincan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mikeal.roose@ucr.edu
                                                                                                                                                                                                                                                                                                                               contaminants, and to trim to a high quality region.
Sequences that retained a phred 17 region of at least 100
bases were deposited to GenBank."
196 C 210 g 243 t
                                                                                                                                                                                                                                                                                                                                                                                                      Core Instrumentation Facility, (Choi, Kingan). Chromatogram files were transmitted to UC Riverside (by Choi), then processed at UC Riverside (by Wanamaker) us: the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Poncirus trifoliata CTV-challenged cDNA library - UCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TJC121"
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/cultivar="Pomeroy
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                                                                                                              Unpublished
Contact: Mikeal Roose
                                                                                                                                                  Development of EST Resources
Citrus - Poncirus trifoliata
                                                                                                                                                                                                                                                                                                                                                                         CD575807.1
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 Seq primer:
                                      Fax: 9097874437
                                                                                                                                                                                                                                                                                                                                 Poncirus trifoliata
                      mikeal.roose@ucr.edu
                                                                                                                                                                                                                                                                                                                                                                         GI:31671709
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122 ACATTTGGAGACTATGGTGGTGGGTGGCCAAAGTGGCCATGCAACTTTCTATGGAGGGGGT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eyermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids II; Sapindales; Rutaceae; Poncirus.

1 (bases 1 to 816)
Roose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D.,
Wanamaker, S., Collura, K., Feuerbacher, O., Kim, H.R., Kudrna, D., Win,
R. and Yu, Y.
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816 bp mRNA linear SST 12-JUN-2003
UCRPT01_01ae06_g3 Poncirus trifoliata CTV-challenged cDNA library -
AGI Poncirus trifoliata cDNA clone UCRPT01_01ae06, mRNA sequence.
Department of Botany & Plant Sciences, University of California Riverside, CA, 92521-0124, USA Tel: 9097874137
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CTV-challenged phloem -
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TGCTATGAAATGAAAATGTGAAAATGACCCCAAGTGGTGCCTCCCCGGCTCCATCATTGTC 376
                                                                                                                             GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
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Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the Ctv resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the Ctv resistance gene. Shoots 10-30 cm long were harvested in october 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using TriZol reagent (Gibco). Poll(A) RNA was gurified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of pelformed in the MI Roose lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wilng, Yu).

Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to
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lab_host="E. coli TJC121"
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clone="UCRPT01_01ae06
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cultivar="Pomeroy OP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="Phloem"
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1153.50
90.65%
83.74%
82.75%
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	FEATURES source			JOURNAL COMMENT	TITLE	REFERENCE AUTHORS		SOURCE	ACCESSION VERSION KEYWORDS	RESULT 3 CB291406 LOCUS DEFINITION	מם	Qy	ממ	Qγ	Db	Qy	dd Q			מם	γ	מם	Qy	₽ 5	
i- in ve	Location/Qualifiers 1809 /organism="Citrus sinensi	Email: timothy.close@ucr.edu Seq primer: T3	7 (0 )	Unpublished Contact: Timothy Close Department of Rotany & Dlant Sciences University of California	Development of EST Resources and New Genetic Markers for California Citrus	1 (bases 1 to 809) Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R., Kidrna D wanamaker C wing B and Vi V	BUKATYOTA; VIIIdIPLANTAE; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus.	Citrus sinensis Citrus sinensis	GON CB291406. CB291406.1 GI:28616863	CB291406  CB291406  CB291406  CB291406  CB291406  CD201		240 GlnPheGlyGlnThrTyr 245	737 CAAGTGACAGCCAGTGACGGAGGACTGTGACTAGCAACAATGTTGTGCCTGGAAATTGG 796	220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrp 239	677 AGGAACTGGGGCCAAAATTGGCAGAGCAATTCTTATCTTAACGGCCAAAGTCTTTCTT	200 ArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPhe 219	180 AlderyAsbyelhisservelserileLyBetSerarinTelyFibelisermetser 199 [	57 AGGITTACCGTCAATGGACACTCATACTTCAACCTGGTTTTGATCACAAATGTCGGAGGA	60 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 1	497 CGTGCCGGTATCGTCCCAATTTCCTTCAGAAGGATCCCGTGTGCGAAGAAAGGAAGG	140 ArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyVal 159	437 AATCCTCCCCTCCAGCACTTTGACATGGCTGAGCCCGCTTTCTTGCAAATTGCCCCAATAC 496	120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139	377 ACCGCCACCAACTTCTGCCCACCTAACCTTGCCCTGTCTAACGACAACGGCGGTTGGTGC 436	ThralaThragaDheCveDroDroAenDhealelenCroAenAenAenClor() vTroCve

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Query Match:
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Best Local Similarity:
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ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 179
                                                                                                                                                                                                                                                                                                                                                                                                                           CysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCTTCCGGCACAATGGGTGCTTGTGGGTATGGCAATTTGTACAGCCAAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyr
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                                                                                       ArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyVal 159
                                                           AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyr 139
                                                                                                                                                                                                                                                                                                                                 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrpCys 119
                                                                                                                                                                                                                                                                                                                                                                                         TGCTATGAAATGAAATGTGAAAATGACCCCAAGTGGTGCCTCCCCGGCTCCATCATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACTAACACTGCATCACTCAGTACCGCTCTATTCAACAATGGCCTAAGCTGTGGTTTCA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda CNNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Penton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura , Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitis vinifera
Vitis vinifera
Vitis vinifera
Lukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; rosidi
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidi
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidi
Vitaceae; Vitis.
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CB980842.1 GI:30304048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 530 754 6561
Fax: 530 754 6617
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One Shields Ave, Davis, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Douglas Cook, PhD CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental stages
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                   192
                                                                          /clone lib="Cabernet Sauvignon Berry Post-Véraison - CAB7"
/note="Organ: Berry; Vector: pDNR; Site 1: Sfil; Site 2:
Sfil; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8
berries. Samples were collected post-veraison from
field-grown vines during stage III of berry growth at 89
days after full bloom. Berries soluble solid concentration
ranged between 18-19 brix. Sampled vines were located at
the University of California, Davis, Experimental
Vineyard. cDNAs were made by oligo-dT priming and directi
onally cloned. 5'and 3' adaptors were used in cloning as
follows: 5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGGCGGAGGTGGGCCGACATG-GT(30)NN-3'. Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drcook@ucdavis.edu
                                   constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction.
                                                                                                                                                                                                                                                                                                                                     /dev_stage="Post-Veraison, 18-19 brix"
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                                               /clone="CAB70003_IIaR_A03"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                              cultivar="Cabernet Sauvignon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="mRNA"
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CB293003.1 GI:20
EST.
Citrus sinensis
Citrus sinensis
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UCRCSO1 05bf07 g1 Washington Navel orange cold acclimated flavedo &
albedo cDNA library Citrus sinensis cDNA clone UCRCS01_05bf07, mRNA
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                                                                                                                                                                                                   SerAsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe
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                                                                                                                                                                                                                                                                                                                                                                    GTGGCCGGAGCGGGAGACGTCAGGGCAGTATCAATAAGGGGGGTCTAAGACCGGGTGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGGGATCCGCTTTACCATCAACGGCCACTCCTACTTCAACTTGGTGCTCATCACAAAC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsn 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGGGGCATGTTACGAGATGAAATGCAACGATGACCCCAAATGGTGCCTCCCAGGGACC
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AUTHORS
                                                       Query Match:
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Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kudrna, D., Wanamaker, S., Wing, R. and Yu, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Botany & Plant
Riverside, CA, 92521-0124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: timothy.close@ucr.
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Timothy Close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                            mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from serveral fruits, then wrapped in aluminum foll and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanases Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and I million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Penton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an All S30 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Yu) anamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
(1-250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library" [Investor of the cold acclimated /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="Rind containing
/dev_stage="Mature fruit"
/lab_host="E. coli TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Washington Navel"
/db_xref="taxon:2711"
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                                                       4.58e-96
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83.13%
81.38%
x CB293003
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Matches:
Conservative:
Mismatches:
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REFERENCE
AUTHORS
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Unpublished
Contact: Carroll P. Vance
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle
Tel: 612 625 5715
                                                                                                                                                                                                                                                         Medicago truncatula

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;

spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;

peurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG581975
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EST483712 GVN Medicago truncatula cDNA clone pGVN-66I24 5' end,
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                                                                                                                                                                                                                                       Medicago.
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                                                                                                                                                 (bases 1 to 798)

(c) Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.

(c) Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.

(c) Ts from one month old nitrogen-fixing root nodules of Medicago
                        Buford Circle,
                        St.Paul,
                        ₹
                        55108
                        USA
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158 GlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnVal
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Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M383038e TIGR sequence name:
MTCDP60TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValPheThrPheAlaAspTyr---GlyGlyTrpGlnSerGlyHisAlaThrPheTyrGly
                                                                                                                                                                                                                                                                                                                                                   GlyAlaCysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGln
                                                                                            GlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGly
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ATGGCAATAGTAGCAACCTCATTCATCTCTATTCTTTTCTTTGTTCTTAGCTTATGCCTT
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                                                                                                                                                                                                                                                                                                                           GGGTCTTGCTACGAGATGAAATGTAACAGTGACCCTAAATGGTGCCTTCCTGGTAGCATA
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/dev stage="effective root nodules harvested one month
/dev stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab host="E. coli strain XLOLR"
/clone lib="GVN"
/clone lib="GVN"
/clone lib="GVN"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
21 a 173 c 175 g 229 t
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/mol type="mRNA"
/cultivar="genotype Al
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive,
Black Mountain, Camberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High
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CD486517
CD486517.1 GI:31407482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium Wilt Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTCGACCCACGCGTCCG):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
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d,C., Wilson,I. and McFadden,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: M13 reverse primer n quality sequence stop: 736.
                                           182
                                           þ
                                                       /note="Vector: Lambda ZIPLOX; Site_1: SalI; Site_2: NotI; mRNA was prepared from root and hypocotyl tissues of the cotton cultivar DeltaEMERALD. cDNA was synthesised from a NotI-oligodT primer/adapter using the manufacturers protocols (Life Technologies) and then ligated to a SalI adapter to facilitate directional cloning. The cDNA was cloned into the SalI and NotI sites of the Lambda ZIPLOX phage vector (Life Technologies). Constructed by Caitriona Dowd and Helen McFadden."
                                                                                                                                                                                                                                                                       /tissue_type="Root and hypocoty1 tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
                                                                                                                                                                                                                                                                                                                                                                organism="Gossypium hirsutum"

/mol_type="mRNA"

/cultivar="DeltaEMERALD"
                                                                                                                                                                                                                                     /clone_lib="Cotton Root and Hypocotyl Lambda
Library (CRH)"
                                                                                                                                                                                                                                                                                                                                  clone="CRH3.3F02"
                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:3635"
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                                                                                                                                                                          CAB70003_IIAF_A03 Cabernet Sauvignon Berry Post-Veraison - CAB vitis vinifera CDNA clone CAB70003_IIAF_A03 5', mRNA sequence. CB980777
     Goes
                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu
                                                                         Vitis vinifera
Eukaryota; Viridiplantae;
                                                                                                                    Vitis vinifera
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Vitaceae; Vitis.
(bases 1 to 772)
oes da Silva, F., I
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Expressed sequence tags from cabernet sedevelopmental stages
Unpublished
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
331
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CTAACCGTGACTGCCACAAACTTCTGCCCTCCTAACTTGGCCTTGTCCAACACCAACGGC
                    IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGly
                                                                                              CysG1yAlaCysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProG1yThr
                                                                                                                                                     CAAGGGTATGGGACCAACACTGCAGCTCTCAGCACCGCTCTCTTCAACAGTGGGCTGAGC
                                                                                                                                                                             GlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSer
                                                                                                                                                                                                                                     GGCGGTGGTGACGCCTCAGGCACAATGGGTGGGGCTTGTGGGGTATGGCAACTTGTACAGC
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                                                                             TGTGGGGCATGTTACGAGATGAAATGCAACGATGACCCCAAATGGTGCCTCCCAGGGACC
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Botany & Plant
Riverside, CA, 92521-0124
Tel: 9097873318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Sapindales; Rutaceae; Citrus.; (bases 1 to 788) (Colura; K., Fenton, R.D., Feuerbacher, O., Kim, H.R., Close, T.J., Collura; K., Fenton, R.D., Feuerbacher, O., Kim, H.R., Eugerbacher, O., Wanamaker, S., Wing, R. and Yu, Y.

Development of EST Resources and New Genetic Markers for Californi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Citrus sinensis
Citrus sinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Contact: Timothy Close
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                                                                                                                                                                                                                                                                                                                                                                                     primer:
/clone="UCRCS01_02af04"
/tlssue_type="Rind containing flavedo and albedo"
/tlssue_type="Rind containing flavedo and albedo"
/tlssue_type="Mature fruit"
/dev stage="Mature fruit"
/lab host="E. coli TJC121"
/lab host="E. coli TJC121"
/clone_lib="Washington Navel orange cold acclimated
flavedo & albedo cDNA library"
/note="Pvector: Lambda Uni-ZAP XR, excised phagemid;
/site_1: EcoRI; Site_2: XhoI; Plants were grown in the
field at University of California, Riverside Agricultural
Operations since 1983. The scion was Washington Navel
orange and the rootstock Carizzo Citrange. Tissue from
mature fruit was harvested at mid-day in January 2002
                                                                                                                                                                                                                                                                                                                                                                                                           timothy.close@ucr.edu
                                                                                                                                                                                                                                                        /organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Washington Navel"
/db_xref="taxon:2711"
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AlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMetSer
                                                                                                      ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly
                                                                                                                                                                                                         ArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGCAGCATCATCTAGCGTTGCTCCTCTTTGTTTGTGCTCAATTTTTGCTTTCGTGGC 135
                                                                           AGGTTTACCGTCAATGGACACTCATACTTCAACCTGGTTTTGGTCACAAATGTCGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA nurified CDNA clones archived and nur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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AUTHORS
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Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Frass
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="flower"
/tissue_type="flower"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/clone_lib="tomato flower, 1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; The
/note="They tomation of the content of the cont
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/clone="cTOC24J22"
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/cultivar="TA496"
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8 mm to preanthesis buds Lycopersicon
)C24J22 5' end, mRNA sequence.
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                                                                                         Unite de genetique et amelioration des fruits et legumes Institut National de la Recherche Agronomique Domaine Saint-Maurice BP 94 84143 Montfavet cedex Tel: 00-33-(0)4-32-72-26-68 Fax: 00-33-(0)4-32-72-26-62
                                                                                                                                                                                                                                                                                                                                                                                                         CB822230
CB822230
EST 3081 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus armeniaca cDNA clone be005k06 3', mRNA sequence.
                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 864)
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                                                                                                                                                                                                     High Throughput Detection of Isogenes Apricot Fruit(Prunus armeniaca)
                                                                                                                                                                                                                                    Grimplet, J., Romieu, C., Audergon, J.M., Albagnac, G., Bouchet, J.P. and Terrier, N.
                                                                                                                                                                                                                                                                                                                                Prunus armeniaca (apricot)
Prunus armeniaca
                                                                           Email: audergon@avignon.inra
                                                                                                                                                                        Contact: Audergon JM
                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuVal
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                                                              primer:
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/organism="Prunus armeniaca"
/mol_type="mRNA"
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                                                                                   MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeu
                                                                                                                                              GlyGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSer
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                                                                                                                            GGAGGTGCAGGGGATGTGCACTCTGTTTCAATCAAGGGGTCCAAAACAGGGTGGCAAGCC
                                                                                                                                                                                           GGGATAAGATTCACCATCAACGGTCACTCTTACTTCAACTTGGTTTTGATCACAAACGTT
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/clone_lib="Half-Ripe Apricot Fruit Lambda Zap II Library"
/clone="Organ: Fruit; Vector: Lambda Zap II; Site 1: Ecc RI
/site_2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeguie-Mbeguie D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: atr01-4ms1 row: d column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 Mueller Laboratory, Department
State University, University Park,
Tel: 814 863 6413
Fax: 814 865 9131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dePamphilis,C., Soltis,D., Soltis,P., Farmerie,W., Ma,H., Tanksle, S., Leebens-Mack,J., Field,D., Buzgo,M., Kim,S., Ilut,D., Landhei, L., Hu,Y., Wall,K., Albert,V., Carlson,J., Doyle,J., Frohlich,M., Miller,W., Oppenheimer,D. and Theissen,G. Generation of ESTs from early flower buds of Amborella trichopoda Unpublished Contact: Claude dePamphilis or James Leebens-Mack Mueller Laboratory
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CD484188.1 GI:31405456
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                                                                                                                                                                       /clone="Vector: pBluescript SK (+/-); Site 1: EcoRI;
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
/note 1: Amborella trickers only. Only floral buds with
diameter of 2.5 mm of less were used for RNA isolation.
This is a directionally cloned, non-normalized library.
Avg. insert length: 1611; Primers: M13F and M13R;
Antibiotic: 50 ug/ml Ampicillin; Primery Titer: 2.24E6 pfu
total; Amplified Titer: 1.37E10 pfu/ml; Mass Excised
Titer: 3.53E9 total; This library has been generated by
the Ploral Genome Project (FGP). We would like to thank
David Lorence at the National Tropical Botanical Garden
for providing plant material for library building. The
Floral Genome Project is funded by NSF's Plant Genome
Research Program (DBI-0115684). More information about the
project can be obtained at http://fgp.bio.psu.edu"
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/db_xref="taxon:13333"
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lab_host="SOLR"
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Contact: Cushman JC
Department of Biochemistry
University of Nevada
                                                                                                                                                        Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
Caryophyllales; Aizoaceae; Mesembryanthemum.
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                                                             Unpublished
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                                                                             Mesembryanthemum
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Plate: L48-11
Seq primer: T3
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Tel: 775-784-1918
Fax: 775-784-1650
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PCR PRimers
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GlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSerMet 198
                                                                                                                                                                                                                                                               ValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTrp
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                                                   ValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGly 178
                                                                                                   AlaCysPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArg
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                                                                                                                        TyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLysLysGlyGly 158
                                                                                                                                                                                                        CysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGln
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EcoRI; Site_2: XhoI"
3 214 c 188 g 211 t
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/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zar, 48 hours NaCl treatment"
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/mol_type="mRNA"
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/clone="L48-1090"
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                                            No : :
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elli

P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,

Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://compgenomics.ucdavis.edu/
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGF20B04, mRNA sequence
BQ990398
BQ990398.1 GI:22409933
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QGF20B04.yg.ab1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig5532, see http://cgpdb.ucfor details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactuca
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                                                                                                                                                                                         /clone lib="QG ERGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, cloned into a custom medium-copy vector and directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                       construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          'lab_host="E.coli"
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/clone="QGF20B04"
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/cultivar="L.serriola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Lactuca sativa"
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egle,J., Ellison
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 Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
Tel: +46 90 786 5279
                                                                                                                                                                                                                                                   BU815493 685 bp mRNA linear N042D11 Populus bark cDNA library Populus tremula tremulaides cDNA 5 prime, mRNA sequence.
                                                     Unpublished Contact: BHALERAO RUPALI R.
                                                                                1 (bases 1 to 685)
Unneberg, P., Bhalerao, R.R., Jar
The poplar tree transcriptome:
from multiple libraries
                                                                                                                                                                                                                                                                                                                                      AsnTrpGlnPheGlyGlnThrTyrGluGlyProGlnPhe
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Email: rupali.bhalerao@plantphys.umu.
Cocation/Qualifiers
1. 685
                                                       GCCCAGTTT
                                                                                                                           ThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGlnThrTyrGluGly
                                                                                                                                                                                SerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArg
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